

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 11, 2005, 06:54:09 ; Search time 112 Seconds
(without alignments)
5654.579 Million cell updates/sec

Title: US-09-994-365-1

Perfect score: 891
Sequence: 1 cccttcgggggtcccgagca.....taaaatcatgtttcttaa 891

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Issued Patents NA: *
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq: *
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq: *
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq: *
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq: *
5: /cgn2_6/ptodata/1/ina/PTCUS_COMB.seq: *
6: /cgn2_6/ptodata/1/ina/backfile1.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	160	18.0	248	US-09-621-976-9776	Sequence 9776, Ap
2	80.8	9.1	7218	US-08-232-463-14	Sequence 14, Appl
3	45.4	5.1	2220	US-08-765-907A-14	Sequence 14, Appl
4	45.4	5.1	4496	US-08-765-907A-6	Sequence 6, Appl
5	44.8	5.0	53526	US-08-658-136-2	Sequence 2, Appl
6	44.8	5.0	53577	US-08-658-136-1	Sequence 1, Appl
7	43.8	4.9	645	US-08-403-852D-9	Sequence 9, Appl
8	43.8	4.9	645	US-08-510-646B-9	Sequence 9, Appl
9	43.8	4.9	645	US-09-231-818-9	Sequence 9, Appl
10	43.8	4.9	645	US-09-635-359B-9	Sequence 9, Appl
11	42.6	4.8	1926	US-09-249-585A-2	Sequence 2, Appl
12	42.6	4.8	1926	US-09-410-389-3	Sequence 3, Appl
13	42.6	4.8	2580	US-09-050-863-2	Sequence 2, Appl
14	42.6	4.8	2580	US-09-359-081-2	Sequence 2, Appl
15	42.6	4.8	5452	US-09-130-114-1	Sequence 1, Appl
16	42.6	4.8	8705	US-09-647-344A-14	Sequence 14, Appl
17	42.6	4.8	9600	US-08-910-647-1	Sequence 1, Appl
18	42.6	4.8	9600	US-09-620-925-1	Sequence 1, Appl
19	42.6	4.8	10596	US-07-884-811-15	Sequence 15, Appl
20	42.6	4.8	10596	US-07-885-971-15	Sequence 15, Appl
21	42.6	4.8	10596	US-08-087-783A-15	Sequence 15, Appl
22	42.6	4.8	10596	US-08-194-088B-15	Sequence 15, Appl
23	42.6	4.8	10596	US-08-194-087-15	Sequence 15, Appl
24	42.6	4.8	10596	BCT-US93-04648-15	Sequence 15, Appl
25	42.6	4.8	16080	US-09-724-566A-48	Sequence 48, Appl
26	42.6	4.8	15231	US-09-128-155-16	Sequence 16, Appl
27	41	4.6	364	US-09-621-976-17202	Sequence 17202, A

28	41	4.6	1166	US-09-072-596-323	Sequence 323, App
29	41	4.6	1166	US-09-072-967-328	Sequence 328, App
30	41	4.6	3297	US-09-620-312D-417	Sequence 417, App
31	39.2	4.4	44377	US-08-804-227C-7	Sequence 7, Appl
32	39.2	4.4	44377	US-08-804-198-1	Sequence 1, Appl
33	38.4	4.3	354	US-09-621-976-13855	Sequence 13855, A
34	38.2	4.3	320	US-09-165-264-7	Sequence 7, Appl
35	37.8	4.2	289	US-09-007-005-17	Sequence 17, Appl
36	37.8	4.2	289	US-09-244-796-17	Sequence 17, Appl
37	37.8	4.2	1660	US-09-697-367-21	Sequence 21, Appl
38	37.8	4.2	1660	US-09-918-909A-21	Sequence 21, Appl
39	37.8	4.2	1738	US-09-918-909A-27	Sequence 27, Appl
40	37.6	4.2	1926	US-09-249-585A-4	Sequence 4, Appl
41	37.6	4.2	1931	US-09-130-114-2	Sequence 2, Appl
42	37.4	4.2	6649	US-09-799-451-384	Sequence 384, App
43	37.2	4.2	711	US-09-252-991A-15345	Sequence 15345, A
44	37.2	4.2	831	US-09-252-991A-15299	Sequence 15299, A
45	37.2	4.2	861	US-09-252-991A-15491	Sequence 15491, A

ALIGNMENTS

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RESULT 1
US-09-621-976-9776/c
; Sequence 9776, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET 054PR2
; CURRENT APPLICATION NUMBER: US/09/621.976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 9776
; LENGTH: 248
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 188
; OTHER INFORMATION: n=a, g, c or t
US-09-621-976-9776

Query Match          18.0%; Score 160; DB 4; Length 248;
Best Local Similarity 93.0%; Pred. No. 8.6e-36;
Matches 173; Conservative 5; Mismatches 5; Indels 3; Gaps 1;

QY 293 CTGAACTGAGATGTGCCCCCTGAACCGCCTTGAAGAGATCTCTTCAACTCCCGGC 352
    |||||
DB 186 CTGAACTGAGATGTGCCCCCTGAACCGCCTTGAAGAGATCTCTTCAACTCCCGGC 127

QY 353 CTGACGACCTTGCGCCGCGAGACCCC--AGCCCCAGAAACCCCTGCGCTCTGCGCC 409
    |||||
DB 126 CTGACGACCTTGCGCCGCGAGACCCCAGACCCCGGAAACCCCTGCGCTCTGCGCC 67

QY 410 CTGAGGTGGAACAACGACCTTCAAGAGAGCCAGACCTTGAACCCAGCCGGGAGAGTACA 469
    |||||
DB 66 CTGAGGTGGAACAACGACCTTCAAGAGAGCCAGACCTTGAACCCAGCCGGGAGAGTACA 7

QY 470 GATTAAT 475
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DB 6 GATTAAT 1

RESULT 2
US-08-232-463-14
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
```

APPLICANT: DORNER, F.
APPLICANT: SCHEFFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESS: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: pTZgpt-Fis
US-08-232-463-14

Query Match	9.1%;	Score 80.8;	DB 1;	Length 7218;
Best Local Similarity	4.9%;	Fred. No. 9,8e-13;		
Matches	19;	Conservative 237;	Mismatches 134;	Indels 0;
		Gaps		
QY	480	TCCCCTGACCCGTTCTGTTCCAGGACATCTACGAGCACACGACGCCCTCTCCACCGCTG	539	

Db	1090	YY	1145	
QY	540	TTCCCGCGAATTTCTTCCCAATTAGCCTATCTCTTAAACCTTTCTCATTCCTCG	599	

Db	1150	YY	1209	
QY	600	TTTATATCGAACCCGTAAGGNGGTTCGATATTTCTGTGCCCCCTCTAGATCAT	659	

Db	1210	YY	1269	
QY	660	ACTTAGTCTCATCATCGCCGCTTTTCTCTGACACCTAAGCTACTCTCTACCTCG	719	

Db	1270	YY	1329	
QY	720	CCTCAGGCGTCGCGCCACCTACTCTCCACCCGGTCTTCTGCCCCGCGATCGCTGG	779	

Db	1330	YY	1389	
QY	780	GCAGGCTATGATCTAGTCCCTTCTGCGACCTGCGCGGCGGAGACATCATAG	839	

Db	1390	YYGGTACCAATTTCTT	1449	
QY	840	TAGACACTGCTGCTTCATGAAACGAA	869	

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Db          1450 ATCTCTTAAGTACTGTCATAGTAGTAA 1479

RESULT 3
US-08-765-907A-14
; Sequence 14, Application US/08765907A
; Patent No. 6352839
; GENERAL INFORMATION:
; APPLICANT: BLANC, Veronique
; APPLICANT: THIBAUT, Denis
; APPLICANT: BAWAS-JACQUES, Nathalie
; APPLICANT: BLANCHET, Francis
; APPLICANT: COUZET, Joel
; APPLICANT: BARRIERE, Jean-Claude
; APPLICANT: DEBUSSCHE, Laurent
; APPLICANT: FAMECHON, Alain
; APPLICANT: PARIS, Jean-Marc
; APPLICANT: DUTRUC-ROSSET, Gilles
; TITLE OF INVENTION: Streptogramins And Method For Preparing Same By
; FILE REFERENCE: Streptogramin genes
; CURRENT APPLICATION NUMBER: US/08765,907A
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 2220
; TYPE: DNA
; ORGANISM: Streptomyces pristinaespiralis
US-08-765-907A-14

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Query Match	5.1%	Score 45.4	DB 3	Length 2220
Best Local Similarity	46.0%	Pred. No. 0.006		
Matches 192	Conservative 0	Mismatches 221	Indels 4	Gaps 1
QY	14	CCAGGCACTCCAGACTCAGCCACCACCTTGGGGGCGCAGTATATAGCATGATTCCTCA	73	
DB	248	CCACCGACACCGACCTGGGCTTCAGCCCGGGGATATACGAATGGACCTGCCGCTGC	307	
QY	74	ACTGGAAGCTCTGGGGATCTGTGCTCTTGGCTGCACACCAAGAGGCACTTCAGGCAAG	133	
DB	308	TGGGGAGTGTGCTTGGGCGACCAAGGCTGTGCTGTGCTGCGCGGCGCGCTGTGCACG	367	
QY	134	AGGCGCAACCCCTCCACCCACCCGCGAGAGACCGAGAGAGAGGCAAGCTTCCCAATTGC	193	
DB	368	CACCTGAACCTTTTTCAGGCGCGC---ACAGCGCAATCCGCGCACAGAGGCGAGGCGCTG	423	
QY	194	CTCAGAGGCCCCCAGTCCCCGGTAGCCCTTGGCCAGGGGCAACCCCTCTTTGAAGATC	253	
DB	424	TTGCGGAACATCCCTCCCGGTGACGCTGTGCTGCATACACTGTGTAACCTTGGGCA	483	
QY	254	CTCGGCTACCCGCGCCAGTGTCTCTGAGAGACTGCTGAATCTGAAGTCTGCGCC	313	
DB	484	CTGCCCCCGACTGTGCGCGCAACCGCCACCGCGGAGGCTGATGCGCGTGC	543	
QY	314	CTGAACGCGCTAGAACGAGTCTCTCAACCTCCCGGCGCTAGAGACCTTGGCCGGGAG	373	
DB	544	CACCGCACTGCGCCGCTTGGCGTGCATTTCCACCAGATGATTCAGACGAAAC	603	
QY	374	GACCCCAAGCCCCAGAAACCCCTGGCTCTCTGCGCTGAGTGTGACACCGACTTC	430	
DB	604	GGCGACCGAGTGTGCGCAACTTCCGGAACCTGTCCCTGCGCGCGGCGGCTCACCGC	660	

RESULT 4

US-08-765-907A-6

; Sequence 6, Application US/08765907A

; Patent No. 6352839

; GENERAL INFORMATION:

; APPLICANT: BLANC, Veronique

; APPLICANT: THIBAUT, Denis

; APPLICANT: BAMS-JACOUES, Nathalie

APPLICANT: BLANCHE, Francis
APPLICANT: COUZET, Joel
APPLICANT: BARRIERE, Jean-Claude
APPLICANT: DEBUSCHON, Laurent
APPLICANT: PAMECHON, Alain
APPLICANT: PARIS, Jean-Marc
APPLICANT: DUTRUC-ROSSER, Gilles
TITLE OF INVENTION: Streptogramins And Method For Preparing Same By
TITLE OF INVENTION: Mutasynthesis
FILE REFERENCE: Streptogramin genes
CURRENT APPLICATION NUMBER: US/08/765,907A
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 6
LENGTH: 4496
TYPE: DNA
ORGANISM: Streptomyces pristinaespiralis
US-08-765-907A-6

Query Match 5.1%; Score 45.4; DB 3; Length 4496;
Best Local Similarity 46.0%; Pred. No. 0.0082;

Matches 192; Conservative 0; Mismatches 221; Indels 4; Gaps 1;

14 CCAGGCAACCCAGACTCAGCCACCCAGCTTTGGGGCCAGTACATAGCCATGATCTCTCA 73
Db 3205 CCACCGACACCGACCTGGGCTCAGCCGCGGGTGATCACCAGATGGAGCTGCGGCTGC 3264
QY 74 ACTGGAAGCTCTGGGGATCTGTCTTTGCTTCTGCAACCAAGGAGATCTCAGGCAAGC 133
Db 3265 TCGGGGTGTCTGGGGCCAGCAGGCTGTGCTGTGCGCGCGCGCTGTCTCCACG 3324
QY 134 AGGGCCACCCCTCTCAACCCAGCCGAGAGACGAGAGAGAGAGAGAGAGAGAGAGAGAG 193
Db 3325 CACCCGACCTCTTCAAGGCGCGC---ACAGCGACATCCGCGACGAGCGGCGGCGCTG 3380
QY 194 CTGAGGAGCCCGGAGTCCCGGAGTACCTTTGGCCAGGAGGAGACCCCTCTCTTGAAGATC 253
Db 3381 TTGGCGAAGATCTCCCTCCCGCTGACCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3440
QY 254 CTCCGCTTACCCGCGCGGAGTGTCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 313
Db 3441 CTCCCGCGGAGCTGCG 3500
QY 314 CTGAACCGCTTGAAGAGAGATCTCTCAACCTCCCGCGCGCGCGCGCGCGCGCGCGCG 373
Db 3501 CACCGCACCTGCGCGCGCTTGGGCTGAGTTCACCCGAGATGATCAGCAGGAAACAC 3560
QY 374 GACCCGAGCCCGCGAGAAACCCCTGAGCTCTGCGCGCGCGCGCGCGCGCGCGCGCG 430
Db 3561 GGCTACCGAGTGTCTGCGCACTTCCGAGACTTCTCTGCGCGCGCGCGCGCGCGCGCG 3617

RESULT 5
US-08-658-136-2
Sequence 2, Application US/08658136
Patent No. 6071717
GENERAL INFORMATION:
APPLICANT: KLINGER, KATHERINE W
APPLICANT: LANDES, GREGORY M
APPLICANT: BURR, TIMOTHY C
APPLICANT: CONNORS, TIMOTHY D
APPLICANT: DACKOWSKI, WILLIAM
APPLICANT: GERMINO, GREGORY
APPLICANT: QIAN, FENG
TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE GENE
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESSES:
ADDRESSEE: GENZYME CORPORATION
STREET: ONE MOUNTAIN ROAD
CITY: FRAMINGHAM
STATE: MASSACHUSETTS
COUNTRY: USA

ZIP: 01701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/658,136
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: LASSEN, ELIZABETH
REGISTRATION NUMBER: 31,845
REFERENCE/DOCKET NUMBER: GEN4-17.8
TELECOMMUNICATION INFORMATION:
TELEPHONE: 508-872-8400
TELEFAX: 508-872-5415
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 53526 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-658-136-2

Query Match 5.0%; Score 44.8; DB 3; Length 53526;
Best Local Similarity 50.0%; Pred. No. 0.037;

Matches 112; Conservative 0; Mismatches 112; Indels 0; Gaps 0;

553 CTTCGCAATTAACCTATCTCTTAACCTTCTCTCAATTCCTGCTTTATTTGAAAC 612
Db 3608 CTCCCTCTCTCTCTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 36067
QY 613 CCGTAGGTGTCTCTCAATTTCTCTGCTCCCTCTCTGAGATCCATCTTATGCTCTAC 672
Db 3608 CCGTCCCT 36127
QY 673 ATGGCCGTTTTTCTCTCTGACGCTTAAAGCTATCTCTACTGCGCTCGAGCGCTCG 732
Db 36128 TTCTTCT 36187
QY 733 GCCCACCTACTCTCCACCGGCTTCTCTGCGCGCGGAGTGGT 776
Db 36188 CTCTCCCT 36231

RESULT 6
US-08-658-136-1
Sequence 1, Application US/08658136
Patent No. 6071717
GENERAL INFORMATION:
APPLICANT: KLINGER, KATHERINE W
APPLICANT: LANDES, GREGORY M
APPLICANT: BURR, TIMOTHY C
APPLICANT: CONNORS, TIMOTHY D
APPLICANT: DACKOWSKI, WILLIAM
APPLICANT: GERMINO, GREGORY
APPLICANT: QIAN, FENG
TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE GENE
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESSES:
ADDRESSEE: GENZYME CORPORATION
STREET: ONE MOUNTAIN ROAD
CITY: FRAMINGHAM
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 01701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/658,136
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: LASSEN, ELIZABETH
REGISTRATION NUMBER: 31,845
REFERENCE/DOCKET NUMBER: GEN4-17, 8
TELECOMMUNICATION INFORMATION:
TELEPHONE: 508-872-8400
TELEFAX: 508-872-5415
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 53577 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-658-136-1

Query Match 5.0%; Score 44.8; DB 3; Length 53577;
Best Local Similarity 50.0%; Pred. No. 0.037;
Matches 112; Conservative 0; Mismatches 112; Indels 0; Gaps 0;

QY 553 CTTCGCAATTAGGCTATCTCTTAAACCTTCTCTCATTCCCTCGGTTTATTGTAAC 612
DB 36003 CTCCTC 36062
QY 613 CCGTAAGTGTGTCTCAATATTCTGTGTCCTCTCTGAGATCAACTTAACTGCTCAC 672
DB 36063 CCGTCCCTC 36122
QY 673 ATGCGCCGTTTCTCTCTGACAGCTTAAGCTTACTCTCTGACCTGCGCTGAGCCTCG 732
DB 36123 TTGCTTCT 36182
QY 733 GCCCACCCTAAGCTCCACCCGAGTCTCTGCGCGGAGATGCT 776
DB 36183 CTTCCCT 36226

RESULT 7
US-08-403-852D-9
Sequence 9, Application US/08403852D
Patent No. 5891695
GENERAL INFORMATION:
APPLICANT: Blanc, Veronique
APPLICANT: Blanc, Francis
APPLICANT: Crouzet, Joel
APPLICANT: Jacques, Nathalie
APPLICANT: Lacroix, Patricia
APPLICANT: Thibault, Denis
APPLICANT: Zagorec, Monique
APPLICANT: Debussche, Laurent
TITLE OF INVENTION: Polypeptides involved in the
TITLE OF INVENTION: Biosynthesis Of Streptogramins, Nucleotide Sequences
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSER: Finnegan, Henderson, Farbow, Garrett & Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/403,852D

FILING DATE: 10-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR 93/00923
FILING DATE: 25-SEP-1993
PRIOR APPLICATION DATA: FR 92/11441
FILING DATE: 25-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03806.0054-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 645 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHEICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: S.pristinaespiralis
FEATURE:
NAME/KEY: CDS
LOCATION: 61..645
OTHER INFORMATION: /product= "gene papa"
US-08-403-852D-9

Query Match 4.9%; Score 43.8; DB 2; Length 645;
Best Local Similarity 46.1%; Pred. No. 0.0097;
Matches 185; Conservative 0; Mismatches 212; Indels 4; Gaps 1;

QY 14 CCAGGCAACCCAGACTAGCCACCCAGCTTTGGGGGCGAGTACATAGCCATGATCTCA 73
DB 248 CCAACGACACCGACCTGAGGCTGACGCGCGGGGTGATACCGAATGAGACTGCGCTGC 307
QY 74 ACTGAAAGCTCCGAGGAGATCTGTGCTTGTGCTGACACACGAGGATCTGAGGAGG 133
DB 308 TCGGGGTGTGCTGGGACACAGGCGCTGTGCTGTGCTGCGCGCGCGGTGCTGACG 367
QY 134 AGGGCCACCCCTCTCAACCCAGACCCGAGAGGACCGAGAGGAGGAGGCTCCCAACTTGC 193
DB 368 CACCGAACCCTTTCAAGGCGC---ACAGGAGATCCGACAGAGGAGGAGGCGCTG 423
QY 194 CTGAGGCCCCCAGTTCCTGCTGACCTTTGSCAGAGGCGACCCCTCTCTTTGAAGATC 253
DB 424 TTGCGAATATCCCTCTCCCGCTGACCGTGTCTGCTACCACTGCTGACCGTCCGCAA 483
QY 254 CTGCGCTACCGGCGCCAGTGTCTGAGGAGACTGTGCTGAACTGAGTGTGCGCCG 313
DB 484 CTGCGCGCGGACCTGTGCGCGCACCGCCACACCGCGAGGAGGAGTGTGCGCGCC 543
QY 314 CTGAACCGCTTGAAGAGATCTCTCAACTCTCCGCGCTGACGACCTTGGCGCGGAG 373
DB 544 CACGCGACCTGTGCGCGCTTGGCGTGTGAGTTCAACCGGATGATGAGCAGGAGAAC 603
QY 374 GACCCAGGCCCCCAAAAACCCCTGCGCTGCGCTGAG 414
DB 604 GGCCACGAGATGTGCGCAACTTCCGCGACCTGTGCGCTGCG 644

RESULT 8
US-08-510-646B-9
Sequence 9, Application US/08510646B
Patent No. 6077699
GENERAL INFORMATION:
APPLICANT: Blanc, Veronique
APPLICANT: Blanc, Francis
APPLICANT: Crouzet, Joel
APPLICANT: Jacques, Nathalie

```

APPLICANT: Lacroix, Patricia
APPLICANT: Thibaut, Denis
APPLICANT: Zagorec, Monique
APPLICANT: Debussche, Laurent
APPLICANT: De Crecy-Lagard, Valerie
TITLE OF INVENTION: Polypeptides Involved In The
TITLE OF INVENTION: Biosynthesis Of Streptogramin, Nucleotide Sequences
TITLE OF INVENTION: Coding For These Polypeptides And Their Use
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flinnegan, Henderson, Farabow, Garrett & Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/510,646B
FILING DATE: 03-AUG-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/403,852
FILING DATE: 10-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR 93/00923
FILING DATE: 25-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 92/11441
FILING DATE: 25-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03806.0054-01000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 645 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: S.pristinaespiralis
FEATURE:
NAME/KEY: CDS
LOCATION: 61..645
OTHER INFORMATION: /product= "gene papa"
--S-08-510-646B-9

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Query Match	4.9%	Score 43.8	DB 3	Length 645
Best Local Similarity	46.1%	Pred. No. 0.0097		
Matches	185	Conservative	0	Mismatches 212
			Indels	4
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QY	14	CCAGGCAACCAGACTCAGCCCACTTCGTTGGGGGCGACATAGCCATGATCTCTCA	73	
Db	248	CCACCGACACCGACTCTGGGGCTCAGCCGCGGGGTATACCGAATGGGACCTGGCGCTCC	307	
QY	74	ACTGGAAGCTCTTGGGGATCCTGTGTCCTTTCCTGCAACACAGAGGATCTTAGGACGCG	133	
Db	308	TGGGGTGTGGCTCTGGGCCACAGGCGCTGTGTGCTCTCTCGCCGCGCCGCTGTCTCAGC	367	
QY	134	AGGGGCACCCCTTCAACCCACCCGCGAGAGACCGAGAGAGGAGGCTCCCAACTTTC	193	
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QY 199 CTGAGGAGCCCCCAGTCCCGGCTAGACCTTTGGGCCAGGGGAGACCCCTCTTTTGAAGATC 253

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QY 254 CTCGCGCTACCCGCCCCAGTCGTCTCTCGAAGAGACTGCTCGAATCTGAGCTTGCGCCC 313

Db 484 CTCGCGCGGAGACTGTGGCGGCCACGCGCCACACCGCGCAGCGGAGAGTGAATGGCGTGC 543

QY 314 CTGAAACCGCTTGAAGACGATCTCTCTCAACTCCCGGACCTGACAGACCTTTGGCGGGCAG 373

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QY 374 GACCCGAGCCCCCAGAAAACCCCTGAGCTCTGACCCCTGAG 414

Db 604 GGCACACCGAGTGTGGCCACATCTCCGCACTGTGCTCTGCG 644

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1      RESULT 9
2      US-09-231-818-9
3      / Sequence 9, Application US/09231818
4      / Patent No. 6171846
5      / GENERAL INFORMATION:
6      / APPLICANT: Blanc, Veronique
7      / APPLICANT: Blanc, Franck
8      / APPLICANT: Crouzet, Joel
9      / APPLICANT: Jacques, Nathalie
10     / APPLICANT: Lacroix, Patricia
11     / APPLICANT: Thibaut, Denis
12     / APPLICANT: Zagorec, Monique
13     / APPLICANT: Debussche, Laurent
14     / APPLICANT: De Crecy-Lagard, Valerie
15     / TITLE OF INVENTION: Polypeptides Involved In The
16     / TITLE OF INVENTION: Biosynthesis Of Streptogramins, Nucleotide Sequences
17     / TITLE OF INVENTION: Coding For These Polypeptides And Their Use
18     / NUMBER OF SEQUENCES: 43
19     / CORRESPONDENCE ADDRESS:
20     / ADDRESSEE: Finnegan, Henderson, Farbow, Garrett & Danner
21     / STREET: 1300 I Street, N.W., Suite 700
22     / CITY: Washington
23     / STATE: D.C.
24     / COUNTRY: USA
25     / ZIP: 20005-3315
26     / COMPUTER READABLE FORM:
27     / MEDIUM TYPE: Floppy disk
28     / COMPUTER: IBM PC compatible
29     / OPERATING SYSTEM: PC-DOS/MS-DOS
30     / SOFTWARE: Patent In Release #1.0, Version #1.30
31     / CURRENT APPLICATION DATA:
32     / APPLICATION NUMBER: US/09/231,818
33     / FILING DATE:
34     / PRIOR APPLICATION DATA:
35     / APPLICATION NUMBER: US/08/403,852
36     / FILING DATE: 10-MAY-1995
37     / APPLICATION NUMBER: PCT/FR 93/00923
38     / FILING DATE: 25-SEP-1993
39     / PRIOR APPLICATION DATA:
40     / APPLICATION NUMBER: FR 92/11441
41     / FILING DATE: 25-SEP-1992
42     / ATTORNEY/AGENT INFORMATION:
43     / NAME: Meyers, Kenneth J.
44     / REGISTRATION NUMBER: 25,146
45     / REFERENCE/DOCKET NUMBER: 03806,0054-00000
46     / TELECOMMUNICATION INFORMATION:
47     / TELEPHONE: (202) 408-4000
48     / TELEFAX: (202) 408-4400
49     / INFORMATION FOR SEQ ID NO: 9:
50     / SEQUENCE CHARACTERISTICS:
51     / LENGTH: 645 base pairs
52     / TYPE: nucleic acid
53     / STRANDEDNESS: double
54     / TOPOLOGY: linear
55     / MOLECULE TYPE: cDNA

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Patent No. 6417002
GENERAL INFORMATION:
APPLICANT: Horlick, Robert
TITLE OF INVENTION: METHOD FOR MAINTENANCE AND SELECTION OF EPISOMES
FILE REFERENCE: 0867/OD905
CURRENT APPLICATION NUMBER: US/09/249,585A
CURRENT FILING DATE: 1999-02-11
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2
LENGTH: 1926
TYPE: DNA
ORGANISM: Epstein Barr Virus
FEATURE:
NAME/KEY: CDS
LOCATION: (1) ..(1926)
OTHER INFORMATION: coding strand of EBNA-1 DNA
US-09-249-585A-2

Query Match 4.8%; Score 42.6; DB 4; Length 1926;
Best Local Similarity 43.6%; Pred. No. 0.035;
Matches 247; Conservative 0; Mismatches 314; Indels 6; Gaps 1;

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QY 488 GCGCTTCTGTTCCAGGCAATCTCCAGGCAACGACCTCTCAACCTTGAATCCCGT 547
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QY 608 TGAACCCGTAAGGAGTGTCTCAATATTCTCTCTCTCTCTCTCTCTCTCTCTCT 667
DB 445 CTGCCCCCT 386
QY 668 CTCAATGCGCCGTTTCTCTCTCTGACAGCTTAACTCTCTCTCTCTCTCTCTCT 727
DB 385 CT 326
QY 728 CTTGCGGCCCACTACTCTCCACCCGG 754
DB 325 CCCCCT 299

RESULT 12
US-09-410-399-3/c
Sequence 3, Application US/09410399
Patent No. 6482587
GENERAL INFORMATION:
APPLICANT: Robertson, Erle S.
APPLICANT: Colter, Murray A.
TITLE OF INVENTION: Methods to Inhibit or Enhance the Binding of Viral DNA
TITLE OF INVENTION: to Genomic Host DNA

FILE REFERENCE: UM-03778
CURRENT APPLICATION NUMBER: US/09/410,399
CURRENT FILING DATE: 1999-10-01
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3
LENGTH: 1926
TYPE: DNA
ORGANISM: Epstein-Barr Virus
US-09-410-399-3

Query Match 4.8%; Score 42.6; DB 4; Length 1926;
Best Local Similarity 43.6%; Pred. No. 0.035;
Matches 247; Conservative 0; Mismatches 314; Indels 6; Gaps 1;

QY 194 CTAGAGGCCCCCGAGTCCCGGTAACCTTGGCAAGGGGACCCCTCTTTGAAGATC 253
DB 805 CCCCCTGCCCCCTCTCTGCTCTCTGCTCTCTGCTCTCTGCTCTCTGCTCTCTG 746
QY 314 CTGAACGCGCTGAGAGGAGATCTCTCAACCTCCCGGCTGAGACCTTGGCGGAG 373
DB 745 CTCTGCTCTCTGCCCCCTCTCTGCTCTCTGCTCTCTGCTCTCTGCTCTCTGCTG 686
QY 374 GACCCAGCCCCCGAGAAACCCCTGCGCTCTCTGCTCTGAGTGAACCGA-----C 427
DB 685 CTCTGCCCCCTCCGCCCCCTCTCTCTCTCTCTGCTCTGCCCCCTCTGCTCTGCTG 626
QY 428 CTGAGAGAGAGCGAGACTTGAACCCACCCCGGAGAGTACAGTAATGAGTCCCTCA 487
DB 625 CTCTGCCCCCTCCGCTCTGCTCTGCTCTCTCTCTCTCTGCTCTCTGCCCCCTCTG 566
QY 488 GCGCTTCTGTTCCAGGCAATCTCCAGGCAACGACCTCTCAACCTTGAATCCCGT 547
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DB 505 CCCCCTGCCCCCTCCGCCCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 446
QY 608 TGAACCCGTAAGGAGTGTCTCAATATTCTCTCTCTCTCTCTCTCTCTCTCTCT 667
DB 445 CTGCCCCCT 386
QY 668 CTCAATGCGCCGTTTCTCTCTCTGACAGCTTAACTCTCTCTCTCTCTCTCTCT 727
DB 385 CT 326
QY 728 CTTGCGGCCCACTACTCTCCACCCGG 754
DB 325 CCCCCT 299

RESULT 13
US-09-050-863-2/c
Sequence 2, Application US/09050863
Patent No. 6114111
GENERAL INFORMATION:
APPLICANT: Lao, Ying
APPLICANT: Hiang, Betty
APPLICANT: Payan, Don
TITLE OF INVENTION: Mammalian Protein Interaction Cloning
TITLE OF INVENTION: System
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hohnach, Test, Albritton & Herbert
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: CA
COUNTRY: USA

ZIP: 94111-4187
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/050,863
 FILING DATE: 30-MAR-1998
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Silva, Robin M.
 REGISTRATION NUMBER: 38,304
 REFERENCE/DOCKET NUMBER: A-65638/DJB/RMS
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 781-1989
 TELEFAX: (415) 949-8711
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2580 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: unknown
 TOPOLOGY: unknown
 MOLECULE TYPE: DNA
 US-09-050-863-2

Query Match 4.8%; Score 42.6; DB 3; Length 2580;
 Best Local Similarity 43.6%; Pred. No. 0.039;
 Matches 247; Conservative 0; Mismatches 314; Indels 6; Gaps 1;

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QY 194 CTCAGAGGCCCCCAGTCCCGGTGACCTTGCCAGGGGACCCCTCTTTGAAGATC 253
DB 1248 CTCCTGCCCCCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTG 1189
QY 254 CTCGCGCTACCCGCCCCAGTCTCTCCCTGAGAGACCTGCTGAATGAGTCTGAGCCC 313
DB 1188 CCCCCTCTGCCCCCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTG 1129
QY 314 CTGAACCCGCTGAAGAGGATCTCTCTCAACTCCCGGCTGAGAGACCTTTGGCCGAG 373
DB 1128 CTCCTGCTGCCCCCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTG 1069
QY 374 GACCCCAAGCCCCAGAAACCCCTGAGCTCTGCCCCCTGAGAGTGAACACGAA-----C 427
DB 1068 CTCCTGCCCCCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTG 1009
QY 428 CTCAGAGAGAGCCAGACTTGAACCCACCCGAGAGAGTACAGATTAATGAGTCCCTCA 487
DB 1008 CTCCTGCCCCCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTG 949
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DB 888 CCCCCTCTGCCCCCTCTGCCCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTG 829
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DB 828 CTGCCCCCTCTCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTG 769
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DB 768 CTCCTCTCTGCTCTGCCCCCTCTGCCCCCTCTGCCCCCTCTCTCTCTCTCTCTCTG 709
QY 728 CTCGAGCCCACTCACTCTCCACCCG 754
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RESULT 14
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Sequence 2, Application US/09359081
 Patent No. 6316223
 GENERAL INFORMATION:
 APPLICANT: Lao, Ying
 Hiang, Betty
 Payan, Don
 TITLE OF INVENTION: Mammalian Protein Interaction Cloning
 SYSTEM
 NUMBER OF SEQUENCES: 5
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
 STREET: 4 Embarcadero Center, Suite 3400
 CITY: San Francisco
 STATE: CA
 COUNTRY: USA
 ZIP: 94111-4187
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/359,081
 FILING DATE: 22-Jul-1999
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/050,863
 FILING DATE: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Silva, Robin M.
 REGISTRATION NUMBER: 38,304
 REFERENCE/DOCKET NUMBER: A-65638/DJB/RMS
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 781-1989
 TELEFAX: (415) 949-8711
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2580 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: unknown
 TOPOLOGY: unknown
 MOLECULE TYPE: DNA
 SEQUENCE DESCRIPTION: SEQ ID NO: 2:
 US-09-359-081-2

Query Match 4.8%; Score 42.6; DB 3; Length 2580;
 Best Local Similarity 43.6%; Pred. No. 0.039;
 Matches 247; Conservative 0; Mismatches 314; Indels 6; Gaps 1;

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QY 194 CTCAGAGGCCCCCAGTCCCGGTGACCTTGCCAGGGGACCCCTCTTTGAAGATC 253
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QY 254 CTCGCGCTACCCGCCCCAGTCTCTCCCTGAGAGACCTGCTGAATGAGTCTGAGCCC 313
DB 1188 CCCCCTCTGCCCCCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTG 1129
QY 314 CTGAACCCGCTGAAGAGGATCTCTCTCAACTCCCGGCTGAGAGACCTTTGGCCGAG 373
DB 1128 CTCCTGCTGCCCCCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTG 1069
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QY 428 CTCAGAGAGAGCCAGACTTGAACCCACCCGAGAGAGTACAGATTAATGAGTCCCTCA 487
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Qy 548 GAATTCCTCCCAATTAGACCTATCTCTTAACCTCTCTCATTCCTCGGTTTATTC 607
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RESULT 15
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/ Sequence 1, Application US/09130114
/ Patent No. 5976807
/ GENERAL INFORMATION:
/ APPLICANT: Horlick, Robert A.
/ APPLICANT: Damej, Bassem B.
/ APPLICANT: Robbline, Alan K.
/ TITLE OF INVENTION: Eukaryotic Cells Stably Expressing Genes
/ TITLE OF INVENTION: From Multiple Transfected Epithomes
/ FILE REFERENCE: 0867/1D903US1
/ CURRENT APPLICATION NUMBER: US/09/130.114
/ CURRENT FILING DATE: 1998-08-06
/ NUMBER OF SEQ ID NOS: 36
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 1
/ LENGTH: 5452
/ TYPE: DNA
/ ORGANISM: VEBNA
/ US-09-130-114-1

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Query Match 4.8%; Score 42.6; DB 2; Length 5452;
Best Local Similarity 43.6%; Pred. No. 0.055;
Matches 247; Conservative 0; Mismatches 314; Indels 6; Gaps 1;

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Qy 374 GACCCGAGCCCCGAGAAACCCCTGAGCTCTGCCCCCTGAGGTGAGACACCGA-----C 427
Db 1737 CTCCTGCCCCCTCTGCCCCCTCTCTGCTCTGCTCTGCCCCCTCTGCTCTGCCCC 1796
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Db 1797 CTCCTGCCCCCTCTGCTCTGCCCCCTCTGCTCTGCCCCCTCTGCTCTGCTGCCC 1856
Qy 488 GCGCTTCTGTTCCAGGAGATCTCAGGACCCAGCCCTCTGCAACCTTGATTCGCCGT 547
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Qy 548 GAATTCCTCCCAATTAGACCTATCTCTTAACCTCTCTCATTCCTCGGTTTATTC 607
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Comugen Ltd.

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	775	87.0	55050	17	US-10-467-752-4
5	773.8	86.8	25235	15	US-10-164-230-2
6	563.4	63.2	565	15	US-10-029-386-5700
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14	56	6.3	891	18	US-10-425-115-146045	Sequence 146045, S
15	52.8	5.9	5452	15	US-10-017-161-1481	Sequence 1481, Ap
16	52.8	5.9	5452	15	US-10-292-798-1189	Sequence 1189, Ap
17	51.8	5.8	671	14	US-10-184-644-346	Sequence 346, App
18	51.8	5.8	671	14	US-10-184-634-346	Sequence 346, App
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20	51.8	5.8	12733	14	US-10-032-393-47	Sequence 47, Appl
21	51.8	5.8	12739	14	US-10-032-393-8	Sequence 8, Appl
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28	46.6	5.2	1117	17	US-10-021-323-9375	Sequence 9375, Ap
29	46.6	5.2	1117	15	US-10-017-161-1403	Sequence 1403, Ap
30	46.6	5.2	1117	15	US-10-292-798-1141	Sequence 1141, Ap
31	46	5.2	822	18	US-10-425-115-102047	Sequence 102047, A
32	45.4	5.1	3594	17	US-10-437-963-51978	Sequence 51978, A
33	45.2	5.1	694	14	US-10-184-644-60	Sequence 60, Appl
34	45.2	5.1	694	14	US-10-184-634-60	Sequence 60, Appl
35	45.2	5.1	712	18	US-10-425-115-118813	Sequence 118813, A
36	45	5.1	706	17	US-10-437-963-17102	Sequence 17102, A
37	45	5.1	805	16	US-10-424-599-61903	Sequence 61903, A
38	45	5.1	940	17	US-10-437-963-40850	Sequence 40850, A
39	44.8	5.0	1327	16	US-10-398-221-1265	Sequence 1265, Ap
40	44.8	5.0	1732	17	US-10-437-963-77232	Sequence 77232, A
41	44.8	5.0	53522	10	US-09-904-968-1	Sequence 1, Appl
42	44.6	5.0	497	16	US-10-424-599-133788	Sequence 133788, A
43	44.4	5.0	766	18	US-10-425-115-82176	Sequence 82176, A
44	44.4	5.0	862	17	US-10-437-963-28390	Sequence 28390, A
45	44.2	5.0	556	18	US-10-363-345A-23585	Sequence 23585, A

ALIGNMENTS

RESULT 1
US-09-994-365-1
Sequence 1, Application US/0994365
Patent No. US20020115148A1
GENERAL INFORMATION:
APPLICANT: Charmley, Patrick
APPLICANT: Moes, Patrick
APPLICANT: Moes, Patrick
TITLE OF INVENTION: Compositions and Methods for Diagnosing or Treating Psoriasis
FILE REFERENCE: CECH18109
CURRENT APPLICATION NUMBER: US/09/994,365
CURRENT FILING DATE: 2001-11-26
PRIOR APPLICATION NUMBER: US 60/253,592
PRIOR FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: US 60/256,839
PRIOR FILING DATE: 2000-12-15
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1
LENGTH: 891
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (64)..(471)
US-09-994-365-1

Query Match 100.0%; Score 891; DB 9; Length 891;
Best Local Similarity 100.0%; Pred. No. 3.4e-258;
Matches 891; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTCTTGAGGTTCCAGGACCACTACAGCCACCCAGCTTTGGGGGCGCATACATA 60
DB 1 CCTCTTGAGGTTCCAGGACCACTACAGCCACCCAGCTTTGGGGGCGCATACATA 60

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QY 61 GCCATGATCCTCACTGGAAGCTCTGGGGATCTGGTCTCTTGGCTGACACACAGAGGC 120
Db 61 GCCATGATCCTCACTGGAAGCTCTGGGGATCTGGTCTCTTGGCTGACACACAGAGGC 120
QY 121 ATCTCAGGACGAGGAGCCACCCCTCTCACCCACCCGAGAGAGCCGAGAGAGGAGGC 180
Db 121 ATCTCAGGACGAGGAGCCACCCCTCTCACCCACCCGAGAGAGCCGAGAGAGGAGGC 180
QY 181 TCCCAACATTGGCTCAGGGGCCCCCAGTCCCGGTGACCTTGGCCAGAGGGGCACCCCCT 240
Db 181 TCCCAACATTGGCTCAGGGGCCCCCAGTCCCGGTGACCTTGGCCAGAGGGGCACCCCCT 240
QY 241 CTCTTGAAGATCTCTCGGCTACCCGCTCAGTGGTCTCTGAGAGAGCTGCTGAACT 300
Db 241 CTCTTGAAGATCTCTCGGCTACCCGCTCAGTGGTCTCTGAGAGAGCTGCTGAACT 300
QY 301 GGAATCTGGCCCTCTGAAACCGCTAGAAAGATCTCTCAACTCTCCCGGCTGAGAC 360
Db 301 GGAATCTGGCCCTCTGAAACCGCTAGAAAGATCTCTCAACTCTCCCGGCTGAGAC 360
QY 361 CCTTGGCCGGGAGAGACCCCAAGCCCCAGAAAACCCCTGGCTCTGAGAGAGCTGCTGAACT 420
Db 361 CCTTGGCCGGGAGAGACCCCAAGCCCCAGAAAACCCCTGGCTCTGAGAGAGCTGCTGAACT 420
QY 421 AACGCACTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
Db 421 AACGCACTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
QY 481 CCCCTCAGCCGCTCTGTTCCCAAGCATCTCCAGGACCCAGCCCTCTCAACTCTGAT 540
Db 481 CCCCTCAGCCGCTCTGTTCCCAAGCATCTCCAGGACCCAGCCCTCTCAACTCTGAT 540
QY 541 TCCCGGGAATCTTCCCAATTTAGCCATCTCTTAAACCTCTTCACTCTGAT 600
Db 541 TCCCGGGAATCTTCCCAATTTAGCCATCTCTTAAACCTCTTCACTCTGAT 600
QY 601 TTATATCTGAACCCGTAAGGTGTCTCAATATTTCTGTCTCCCTCTGAGATCATA 660
Db 601 TTATATCTGAACCCGTAAGGTGTCTCAATATTTCTGTCTCCCTCTGAGATCATA 660
QY 661 CTTAGTCTCAGATGCGCCGTTTTTTCTCTGAGAGGCTTAACTCTCTTCACTGAT 720
Db 661 CTTAGTCTCAGATGCGCCGTTTTTTCTCTGAGAGGCTTAACTCTCTTCACTGAT 720
QY 721 CTCAGGCTGCGGCCCACTACCTCCACCCGCTCTTCTGCGCGGAGATCGCTGGG 780
Db 721 CTCAGGCTGCGGCCCACTACCTCCACCCGCTCTTCTGCGCGGAGATCGCTGGG 780
QY 781 CAGGCTATGCTATGTTCTCTTCTGCACTGTGTGGCGGAGAGAGAGATCAGT 840
Db 781 CAGGCTATGCTATGTTCTCTTCTGCACTGTGTGGCGGAGAGAGATCAGT 840
QY 841 AGACAGCTGCTGCTTCCATGAAAGGAAAAATTAATATCATGTTTCTTAA 891
Db 841 AGACAGCTGCTGCTTCCATGAAAGGAAAAATTAATATCATGTTTCTTAA 891

RESULT 2
US-09-994-365-10
; Sequence 10, Application US/09994365
; Patent No. US20020115148A1
; GENERAL INFORMATION:
; APPLICANT: Charmley, Patrick
; APPLICANT: Moss, Patrick
; APPLICANT: McEuen, Mark
; TITLE OF INVENTION: Compositions and Methods for Diagnosing or Treating Psoriasis
; FILE REFERENCE: CECH118109
; CURRENT APPLICATION NUMBER: US/09/994,365
; PRIOR FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: US 60/253,592
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 60/256,839
; PRIOR FILING DATE: 2000-12-15
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; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10
; LENGTH: 2997
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-994-365-10

Query Match      87.0%; Score 775.4; DB 9; Length 2997;
Best Local Similarity 99.9%; Pred. No. 3,4e-223;
Matches 776; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 115 AGAGGATCTCAGGACAGGAGGAGCCCTCTTACCCACCTGCAAGAGAGAGAG 174
Db 2198 AGAGGATCTCAGGACAGGAGGAGCCCTCTTACCCACCTGCAAGAGAGAGAG 2257
QY 175 GCAAGCTCCCCAATTGGCTCAGGGCCCCCAGTCCCGGTGACCTTGGCCAGGGGCA 234
Db 2258 GCAAGCTCCCCAATTGGCTCAGGGCCCCCAGTCCCGGTGACCTTGGCCAGGGGCA 2317
QY 235 CCCCTCTCTTGAAGATCTCCGCTACCCGCTCAGTGGTCTGAGAGAGAGAGAG 294
Db 2318 CCCCTCTCTTGAAGATCTCCGCTACCCGCTCAGTGGTCTGAGAGAGAGAGAG 2377
QY 295 GAAACTGAGTCTGAGCCCTCTGAAACCGCTTAAAGAGATCTCTCAACTCTCCCGGCT 354
Db 2378 GAAACTGAGTCTGAGCCCTCTGAAACCGCTTAAAGAGATCTCTCAACTCTCCCGGCT 2437
QY 355 GAGACCTCTTGGCCGGGAGAGACCCCAAGCCCCAGAAAACCCCTGGCTCTGAG 414
Db 2438 GAGACCTCTTGGCCGGGAGAGACCCCAAGCCCCAGAAAACCCCTGGCTCTGAG 2497
QY 415 GTGACAAACGCACTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 474
Db 2498 GTGACAAACGCACTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2557
QY 475 TGAAGTCCCTCAGCCGCTCTGTTCCCAAGCATCTCCAGGACCCAGCCCTCTCACT 534
Db 2558 TGAAGTCCCTCAGCCGCTCTGTTCCCAAGCATCTCCAGGACCCAGCCCTCTCACT 2617
QY 535 TCGATTTCCCGGAATCTTCCCAATTTAGCCATCTCTTAAACCTCTTCACTTCC 594
Db 2618 TCGATTTCCCGGAATCTTCCCAATTTAGCCATCTCTTAAACCTCTTCACTTCC 2677
QY 595 CTGGTTTATCTGAACCCGTAAGGTGTCTCAATATTTCTGTCTCCCTCTGAGA 654
Db 2678 CTGGTTTATCTGAACCCGTAAGGTGTCTCAATATTTCTGTCTCCCTCTGAGA 2737
QY 655 TCCATATTAATGCTCAGATGCGCCGTTTTTTCTCTGAGAGGCTTAACTCTCTTA 714
Db 2738 TCCATATTAATGCTCAGATGCGCCGTTTTTTCTCTGAGAGGCTTAACTCTCTTA 2797
QY 715 CTGCGCTCAGGCTGCGGCCCACTACCTCCACCCGCTCTTCTGCGCGGAGATCG 774
Db 2798 CTGCGCTCAGGCTGCGGCCCACTACCTCCACCCGCTCTTCTGCGCGGAGATCG 2857
QY 775 CTGGGAGAGGCTATGCTATGTTCTCTTCTGCACTGTGTGGCGGAGAGAGACT 834
Db 2858 CTGGGAGAGGCTATGCTATGTTCTCTTCTGCACTGTGTGGCGGAGAGAGACT 2917
QY 835 ATCAGTGAAGCTGCTGCTTCCATGAAAGGAAAAATTAATATCATGTTTCTTAA 891
Db 2918 ATCAGTGAAGCTGCTGCTTCCATGAAAGGAAAAATTAATATCATGTTTCTTAA 2974

RESULT 3
US-09-994-365-4
; Sequence 4, Application US/09994365
; Patent No. US20020115148A1
; GENERAL INFORMATION:
; APPLICANT: Charmley, Patrick
; APPLICANT: Moss, Patrick
; APPLICANT: McEuen, Mark
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/ TITLE OF INVENTION: Compositions and Methods for Diagnosing or Treating Psoriasis
/ FILE REFERENCE: CECH118109
/ CURRENT APPLICATION NUMBER: US/09/994,365
/ CURRENT FILING DATE: 2001-11-26
/ PRIOR APPLICATION NUMBER: US 60/253,592
/ PRIOR FILING DATE: 2000-11-28
/ PRIOR APPLICATION NUMBER: US 60/256,839
/ PRIOR FILING DATE: 2000-12-15
/ NUMBER OF SEQ ID NOS: 16
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 4
/ LENGTH: 3001
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ US-09-994-365-4

Query Match 87.0%; Score 775.4; DB 9; Length 3001;
Best Local Similarity 99.9%; Pred. No. 3,4e-223;
Matches 776; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 115 AGAGGCAATCTCAGGCGAGGAGGCGACCCCTCTGACCCACCCGAGAGGAGCGAGAG 174
DB 2202 AAGGCAATCTCAGGCGAGGAGGCGACCCCTCTGACCCACCCGAGAGGAGCGAGAG 2261
QY 175 GAGGCTCCCCCAATTGCTCAGGCGCGCCCACTCCCGGTGACCTTGCGCGAGGAGCA 234
DB 2262 GAGGCTCCCCCAATTGCTCAGGCGCGCCCACTCCCGGTGACCTTGCGCGAGGAGCA 2321
QY 235 CCCCCTCTTTGAAAGATCTCGGCTTACCCGCGCCAGTGTCTCTGAGAGACTTGCT 294
DB 2322 CCCCCTCTTTGAAAGATCTCGGCTTACCCGCGCCAGTGTCTCTGAGAGACTTGCT 2381
QY 295 GAAAGTGAATCTGGCGCGCCCTGAAACCGCTAGAAAGATCTCTCAACCTCCCGGCT 354
DB 2382 GAAAGTGAATCTGGCGCGCCCTGAAACCGCTAGAAAGATCTCTCAACCTCCCGGCT 2441
QY 355 GAGGACCTTGGCGCGAGGAGCGCCAGCCCGCAGAAAAACCTGAGCTCTGCGCTGAG 414
DB 2442 GAGGACCTTGGCGCGAGGAGCGCCAGCCCGCAGAAAAACCTGAGCTCTGCGCTGAG 2501
QY 415 GTGGACAACCGACTCAGAGAGAGCCAGACTTAGACCCACCCGCGAGAGTAA 474
DB 2502 GTGGACAACCGACTCAGAGAGAGCCAGACTTAGACCCACCCGCGAGAGTAA 2561
QY 475 TGAAGTCCCTCAGCGGCTTCTGTCGAGGATCTCAGAGACCCAGGCTCTCCAGCC 534
DB 2562 TGAAGTCCCTCAGCGGCTTCTGTCGAGGATCTCAGAGACCCAGGCTCTCCAGCC 2621
QY 535 TCTGAATCCCCGAGAAATTTCCCAATTAGCTATCTCTTAACCTTCTCTCATTTCC 594
DB 2622 TCTGAATCCCCGAGAAATTTCCCAATTAGCTATCTCTTAACCTTCTCTCATTTCC 2681
QY 595 CTCGGTTTATTTGAAACCGGTAAAGTGTGTCTCAATATTTCTGTCCCTCTGAGA 654
DB 2682 CTCGGTTTATTTGAAACCGGTAAAGTGTGTCTCAATATTTCTGTCCCTCTGAGA 2741
QY 655 TCCATATTAGTCTCTCAGATGCGCGGTTTTTCTCTGACAGCTTAAGCTACTCTCTA 714
DB 2742 TCCATATTAGTCTCTCAGATGCGCGGTTTTTCTCTGACAGCTTAAGCTACTCTCTA 2801
QY 715 CCTGCGCTCAGAGGCTCGGCGCCCACTACCTCCAGCCGGTCTTCTGCGCGCGAGATCG 774
DB 2802 CCTGCGCTCAGAGGCTCGGCGCCCACTACCTCCAGCCGGTCTTCTGCGCGCGAGATCG 2861
QY 775 CTGGGGGAGGAGCTATGCTATGTTCTCTTCTGCACTGTGTGCGCGCGAGAACT 834
DB 2862 CTGGGGGAGGAGCTATGCTATGTTCTCTTCTGCACTGTGTGCGCGCGAGAACT 2921
QY 835 ATCAGTGAAGAGCTGCTGCTTCTCAGTGAAGGAGAAAAATCAATGTTTTCTTAA 891
DB 2922 ATCAGTGAAGAGCTGCTGCTTCTCAGTGAAGGAGAAAAATCAATGTTTTCTTAA 2978

RESULT 4
US-10-467-752-4
/ Sequence 4, Application US/10467752
/ Publication No. US20040161759A1
/ GENERAL INFORMATION:
/ APPLICANT: Lench, et al.
/ TITLE OF INVENTION: Test and Model for Inflammatory disease
/ FILE REFERENCE: 2003882-009
/ CURRENT APPLICATION NUMBER: US/10/467,752
/ CURRENT FILING DATE: 2003-08-13
/ PRIOR APPLICATION NUMBER: PCT/GB02/00653
/ PRIOR FILING DATE: 2002-02-13
/ PRIOR APPLICATION NUMBER: GB0103514.6
/ PRIOR FILING DATE: 2001-02-13
/ NUMBER OF SEQ ID NOS: 109
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 4
/ LENGTH: 55050
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (13351)..(13351)
/ OTHER INFORMATION: n is a or t or g or c
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (13401)..(13401)
/ OTHER INFORMATION: n is a or t or g or c
US-10-467-752-4

Query Match 87.0%; Score 775; DB 17; Length 55050;
Best Local Similarity 99.7%; Pred. No. 9,4e-223;
Matches 775; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 115 AGAGGCAATCTCAGGCGAGGAGCGACCCCTCTGACCCACCCGAGAGGAGCGAGAG 174
DB 27096 AAGGCAATCTCAGGCGAGGAGCGACCCCTCTGACCCACCCGAGAGGAGCGAGAG 27155
QY 175 GAGGCTCCCCCAATTGCTCAGGCGCGCCCACTCCCGGTGACCTTGCGCGAGGAGCA 234
DB 27156 GAGGCTCCCCCAATTGCTCAGGCGCGCCCACTCCCGGTGACCTTGCGCGAGGAGCA 27215
QY 235 CCCCCTCTTTGAAAGATCTCGGCTTACCCGCGCCAGTGTCTCTGAGAGACTTGCT 294
DB 27216 CCCCCTCTTTGAAAGATCTCGGCTTACCCGCGCCAGTGTCTCTGAGAGACTTGCT 27275
QY 295 GAAAGTGAATCTGGCGCGCCCTGAAACCGCTAGAAAGATCTCTCACTCCCGGCT 354
DB 27276 GAAAGTGAATCTGGCGCGCCCTGAAACCGCTAGAAAGATCTCTCACTCCCGGCT 27335
QY 355 GAGGACCTTGGCGCGAGGAGCGCCAGCCCGCAGAAAAACCTGAGCTCTCCGCGCTGAG 414
DB 27336 GAGGACCTTGGCGCGAGGAGCGCCAGCCCGCAGAAAAACCTGAGCTCTCCGCGCTGAG 27395
QY 415 GTGGACAACCGACTCAGAGAGAGCCAGACTTAGACCCACCCGCGAGAGTAA 474
DB 27396 GTGGACAACCGACTCAGAGAGAGCCAGACTTAGACCCACCCGCGAGAGTAA 27455
QY 475 TGAAGTCCCTCAGCGGCTTCTGTCGAGGATCTCAGGACCGACGCGCTCTCAACC 534
DB 27456 TGAAGTCCCTCAGCGGCTTCTGTCGAGGATCTCAGGACCGACGCGCTCTCAACC 27515
QY 535 TCTGAATCCCCGAGAAATTTCCCAATTAGCTATCTCTTAACCTTCTCTCATTTCC 594
DB 27516 TCTGAATCCCCGAGAAATTTCCCAATTAGCTATCTCTTAACCTTCTCTCATTTCC 27575
QY 595 CTCGGTTTATTTGAAACCGGTAAAGTGTGTCTCAATATTTCTGTCCCTCTGAGA 654
DB 27576 CTCGGTTTATTTGAAACCGGTAAAGTGTGTCTCAATATTTCTGTCCCTCTGAGA 27635
QY 655 TCCATATTAGTCTCTCAGATGCGCGGTTTTTCTCTGACAGCTTAAGCTACTCTCTA 714
DB 27636 TCCATATTAGTCTCTCAGATGCGCGGTTTTTCTCTGACAGCTTAAGCTACTCTCTA 27695

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.82
 OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.82
 OTHER INFORMATION: SWISSPROT HIT: Q99715, EVALU6 6.20e-01
 OTHER INFORMATION: EST_HUMAN HIT: BF513178.1, EVALU6 0.00e+00
 OTHER INFORMATION: NT HIT: g15304354, EVALU6 0.00e+00
 US-10-029-386-5700

Query Match 63.2%; Score 563.4; DB 15; Length 565;
 Best Local Similarity 99.8%; Pred. No. 1.9e-159;
 Matches 564; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 235 CCCCCTCTTTGGAAGTCTCCGCTACCCGCCAGTGTCTCTGAGAGACTGTCT 294
 Db 1 CCCCCTCTCTTTGGAAGTCTCCGCTACCCGCCAGTGTCTCTGAGAGACTGTCT 60
 QY 295 GAAACTGGAAGTCTGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 354
 Db 61 GAAACTGGAAGTCTGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
 QY 355 GACGACCTTGGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 414
 Db 121 GACGACCTTGGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
 QY 415 GTGGAACAACGAGCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATTA 474
 Db 181 GTGGAACAACGAGCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATTA 240
 QY 475 TGGAGTCTCCCTCAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 534
 Db 241 TGGAGTCTCCCTCAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
 QY 535 TCTGATTCCTCCGTAATCTCTCCCAATTAGCTATCTCTTAACCTCTCTCAATCC 594
 Db 301 TCTGATTCCTCCGTAATCTCTCCCAATTAGCTATCTCTTAACCTCTCTCAATCC 360
 QY 595 CTCGGTTTATCTGAAACCGGTAAAGTGTCTCAATATTTCTGCTCCCTGAGA 654
 Db 361 CTCGGTTTATCTGAAACCGGTAAAGTGTCTCAATATTTCTGCTCCCTGAGA 420
 QY 655 TCCATATTAGTCTCATATGCCCCGTTTTTCTCTGACAGCTTAAGCTACTCTCTA 714
 Db 421 TCCATATTAGTCTCATATGCCCCGTTTTTCTCTGACAGCTTAAGCTACTCTCTA 480
 QY 715 CCTGCTCCAGAGCTCTGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 774
 Db 481 CCTGCTCCAGAGCTCTGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
 QY 775 CTGGGAGAGGCTATGTACTGTGT 799
 Db 541 CTGGGAGAGGCTATGTACTGTGT 565

RESULT 7

US-10-312-841-1/c
 Sequence 1, Application US/10312841
 Publication No. US20030186277A1
 GENERAL INFORMATION:
 APPLICANT: Epigenomics AG
 TITLE OF INVENTION: Diagnose von bedeutenden genetischen Parametern innerhalb des MHC
 FILE REFERENCE: E01/1208/WO
 CURRENT APPLICATION NUMBER: US/10/312, 841
 CURRENT FILING DATE: 2002-12-30
 NUMBER OF SEQ ID NOS: 2
 SEQ ID NO 1
 LENGTH: 3673778
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURES:
 OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
 NAME/KEY: unsure
 LOCATION: (3294164)
 US-10-312-841-1

Query Match 62.6%; Score 557.8; DB 15; Length 3673778;
 Best Local Similarity 82.4%; Pred. No. 9e-157;
 Matches 640; Conservative 0; Mismatches 137; Indels 0; Gaps 0;

QY 115 AGAGGATCTCAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 174
 Db 1426053 ACAAGATCTCAACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1425994
 QY 175 GCAGGCTCCCAAGATGCTCAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAG 234
 Db 1425993 ACAAGATCTCAACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1425934
 QY 235 CCCCCTCTTTGGAAGTCTCCGCTACCCGCCAGTGTCTCTGAGAGAGACTGTCT 294
 Db 1425933 CCCCCTCTCTTTAAAGATCTCCGCTACCCGCCAGTGTCTCTTAAAGAGAGAG 1425874
 QY 295 GAAACTGGAAGTCTGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 354
 Db 1425873 GAAACTGGAAGTCTGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1425814
 QY 355 GACGACCTTGGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 414
 Db 1425813 GACGACCTTGGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1425754
 QY 415 GTGGAACAACGAGCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATTA 474
 Db 1425753 GTGGAACAACGAGCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATTA 1425694
 QY 475 TGGAGTCTCCCTCAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 534
 Db 1425693 TGGAGTCTCCCTCAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1425634
 QY 535 TCTGATTCCTCCGTAATCTCTCCCAATTAGCTATCTCTTAACCTCTCTCAATCC 594
 Db 1425633 TCTGATTCCTCCGTAATCTCTCCCAATTAGCTATCTCTTAACCTCTCTCAATCC 1425574
 QY 595 CTCGGTTTATCTGAAACCGGTAAAGTGTCTCAATATTTCTGCTCCCTGAGA 654
 Db 1425573 CTCGGTTTATCTGAAACCGGTAAAGTGTCTCAATATTTCTGCTCCCTGAGA 1425514
 QY 655 TCCATATTAGTCTCATATGCCCCGTTTTTCTCTGACAGCTTAAGCTACTCTCTA 714
 Db 1425513 TCCATATTAGTCTCATATGCCCCGTTTTTCTCTGACAGCTTAAGCTACTCTCTA 1425454
 QY 715 CCTGCTCCAGAGCTCTGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 774
 Db 1425453 CCTGCTCCAGAGCTCTGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1425394
 QY 775 CTGGGAGAGGCTATGTACTGTGT 799
 Db 1425393 CTGGGAGAGGCTATGTACTGTGT 1425334
 QY 835 ATCAGTGAAGAGCTGTCTCTTCCATGAAGAGAGAGAGAGAGAGAGAGAGAG 891
 Db 1425333 ATCAGTGAAGAGCTGTCTCTTCCATGAAGAGAGAGAGAGAGAGAGAGAG 1425277

RESULT 8

US-10-312-841-2
 Sequence 2, Application US/10312841
 Publication No. US20030186277A1
 GENERAL INFORMATION:
 APPLICANT: Epigenomics AG
 TITLE OF INVENTION: Diagnose von bedeutenden genetischen Parametern innerhalb des MHC
 FILE REFERENCE: E01/1208/WO
 CURRENT APPLICATION NUMBER: US/10/312, 841
 CURRENT FILING DATE: 2002-12-30
 NUMBER OF SEQ ID NOS: 2
 SEQ ID NO 2
 LENGTH: 3673778
 TYPE: DNA
 ORGANISM: Artificial Sequence

FEATURE:
NAME/KEY: modified_base
LOCATION: (139)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (146)..(148)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (151)..(152)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (155)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (172)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (179)..(180)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (182)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (185)..(188)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (192)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (194)..(195)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (210)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (212)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (214)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (219)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (222)..(225)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (229)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (231)..(232)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (238)..(239)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:

NAME/KEY: modified_base
LOCATION: (242)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (245)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (248)..(260)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (265)..(270)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (272)..(276)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
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RESULT 11
US-10-292-798-1191/c
; Sequence 1191, Application US/10292798

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/ Publication No.: US2003023583A1
/ GENERAL INFORMATION:
/ APPLICANT: SUMA, MAKIKO
/ APPLICANT: ASAI, KIYOSHI
/ APPLICANT: AKIYAMA, YUTAKA
/ APPLICANT: ABURATANI, HIROYUKI
/ TITLE OP INVENTION: GUANOSINE TRIPHOSPHATE- BINDING PROTEIN COUPLD RECEPTORS
/ FILE REFERENCE: 084335/166
/ CURRENT APPLICATION NUMBER: US/10/292,798
/ PRIOR FILING DATE: 2002-11-13
/ PRIOR FILING DATE: 2001-12-18
/ PRIOR APPLICATION NUMBER: JP 2001-246789
/ PRIOR FILING DATE: 2001-06-18
/ NUMBER OF SEQ ID NOS: 2070
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 1191
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LOCATION: (311) ..(313)	

OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (323)..(334)
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Matches 207; Conservative	0;	Mismatches 413;	Indels 0;	Gaps 0;

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QY	192	GCTCAGAGGCCCCCAGTCCCGGTGACCTTTGGCAGAGGACCCCTCTCTTTGAGA	251
Db	923	CCNCNCNCCCCCCCCCCCCCNNNNNCCCCCCCCCNCNCCGCCCCCCCCCCCN	864
QY	252	TCTTCGCGCTACCGCGCCCAGTCCGTCCCTGAGAGACCTGCCTGAAACTGAGTCTGGCC	311
Db	863	NCCCCCCCNCCCCCCCNCCCCCCCCCCCCCNNNNCCCCCCCCCCCCCNNNNNCCCC	804
QY	312	CCCTGACCGGCTAAGAGGATCTCTCTCAACCTTCCCGGCTGACGACGCTTGGCGCGC	371
Db	803	CCCCCCCCCNCCCCCNCCNCCCCCNCCCCCCCCCNCCNCCNCCNCCCCCCCCCN	744

[illegible]

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 11, 2005, 06:07:34 ; Search time 540 Seconds
(without alignments)

8661.545 Million cell updates/sec

Title: US-09-994-365-1

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Sequence: 1 ccctctggggtcccgagca.....taaatcatgtttcttaa 891

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	891	100.0	891	6	ABK86962 Human can
2	886.2	99.5	1473	6	ABN60006 Novel hum
3	775.4	87.0	2997	6	ABK86967 Human CAN
4	775.4	87.0	3001	6	ABK86963 Human can
5	775	86.8	55050	4	ABQ75680 Human SER
6	773.8	86.8	25235	4	AAH45310 Human SER
7	563.4	63.2	565	12	ACH72505 Human gen
8	157	17.6	157	12	ACH86315 Human gen
9	61.8	6.9	3133	10	ADCB6738 Human GPC
10	60	6.7	60	6	ABN32329 Human bpl
11	55	6.2	1337	2	AAZ17263 Human gen
12	53	5.9	1218	3	AAA02488 Human col
13	52.8	5.9	5452	10	ADCB6736 Human GPC
14	51.8	5.8	12733	6	ABK96631 Vector pr
15	51.8	5.8	12733	6	ACD13882 L. lactis
16	51.8	5.8	12739	6	ABK98592 Vector ps
17	51.8	5.8	12739	9	ACD13843 Plasmid p
18	50.4	5.7	3163	10	ADCB7060 Human her
19	50	5.6	50	6	ABZ00541 Human leu
20	48.8	5.5	1359	2	AAZ17254 Human gen
21	48.4	5.4	1833	4	ABL22159 Drosophila

C	22	48.2	5.4	1000	3	AAA02484
C	23	47	5.3	1064	6	ABT09678
C	24	46.6	5.2	1117	10	ADCB6688
C	25	46.2	5.2	10732	3	AAA10594
C	26	45.4	5.1	4496	2	AAT58553
C	27	44.8	5.0	1327	6	ABQ68452
C	28	44.8	5.0	53522	2	AAD30228
C	29	44.8	5.0	53526	2	AAT94101
C	30	44.8	5.0	53577	2	AAT18551
C	31	44.8	5.0	53577	2	AAT94108
C	32	44.2	5.0	556	6	ABQ6994
C	33	44.2	5.0	556	6	ABQ6995
C	34	44.2	5.0	1050	6	AAD21685
C	35	44.2	5.0	2849	4	AAD21684
C	36	43.6	4.9	1384	10	ADC87450
C	37	43	4.8	1459	3	AAA02528
C	38	42.8	4.8	2000	8	ADA71938
C	39	42.6	4.8	799	2	AAV55831
C	40	42.6	4.8	1926	4	AAA50254
C	41	42.6	4.8	1926	4	AAFB2902
C	42	42.6	4.8	1926	10	ADK65580
C	43	42.6	4.8	2580	3	AAI75454
C	44	42.6	4.8	2580	6	AAI64275
C	45	42.6	4.8	3198	2	AAK02974

ALIGNMENTS

RESULT 1	ABK86962	standard; cDNA; 891 BP.
ID	ABK86962	standard; cDNA; 891 BP.
XX	ABK86962;	
AC	24-SEP-2002	(first entry)
DT	24-SEP-2002	(first entry)
XX	Human candidate coding sequence-1 (CAN-1) cDNA.	
DE	Human candidate coding sequence-1 (CAN-1) cDNA.	
XX	Human; antipariatic; chromosome 6; candidate coding sequence-1; CAN-1;	
KW	SEK-1; STG; human leukocyte antigen C; HLA C; HLA Cw6; psoriasis; skin;	
KW	keratinocyte; chronic inflammatory dermatosis; erythroderma; seboreic;	
KW	gutrate; pustular variant; Reiter's disease; hyperproliferation;	
KW	epidermis; differentiation; diagnosis; gene therapy; gene; ss; SNP;	
KW	single nucleotide polymorphism.	
XX	Homo sapiens.	
OS	Homo sapiens.	
XX	Location/Qualifiers	
FT	Key	64..474
FT	CDS	64..474
FT	sig_peptide	/tag= a
FT	sig_peptide	/product= "CAN-1"
FT	mat_peptide	/tag= b
FT	mat_peptide	130..471
FT	variation	/tag= c
FT	variation	/note= "Mature CAN-1"
FT	variation	replace(311,C)
FT	variation	/tag= d
FT	variation	/standard_name= "Single nucleotide polymorphism"
PN	WO200244375-A2.	
XX	06-JUN-2002.	
XX	27-NOV-2001; 2001WO-US044506.	
PF	28-NOV-2000; 2000US-0253592P	
XX	15-DEC-2000; 2000US-0256839P.	
PR	(CELL-) CELLTECH R & D INC.	
XX	Charmley P, Moss P, Mceuen M;	
PA	Charmley P, Moss P, Mceuen M;	
XX	Charmley P, Moss P, Mceuen M;	
PI	Charmley P, Moss P, Mceuen M;	

XX MPI; 2002-508513/54.
 DR P-PSDB; AAU79579.
 XX
 PT Novel isolated CAN-1 polypeptide involved in keratinocyte proliferation
 and differentiation, and polynucleotides encoding the polypeptide, useful
 for diagnosing or predicting susceptibility to psoriasis in individual.
 XX
 PS Claim 8; Page 80-81; 95pp; English.

XX The invention discloses isolated candidate coding sequence-1 (CAN-1),
 CC SEER-1 (not defined) and STG (not defined) polypeptides, and the
 CC polynucleotides encoding them. All three genes were identified due to
 CC their proximity to the human leukocyte antigen C (HLA C) locus on
 CC chromosome 6. The HLA Cw6 allele is associated with psoriasis and as the
 CC three genes are expressed in normal skin and/or keratinocyte tissue, they
 CC may also have a role in psoriasis. Psoriasis is a chronic inflammatory
 CC dermatosis that is characterized by hyperproliferation of epidermal
 CC cells. Possible treatments against psoriasis involve the inhibition of
 CC movement of cells into the epidermis, or the inhibition of
 CC hyperproliferation or abnormal differentiation of keratinocytes, by the
 CC inhibition of the CAN-1, STG or SEER-1 polypeptides binding to their
 CC binding partners. The polypeptides are useful for diagnosing or
 CC predicting the susceptibility to psoriasis in an individual, for
 CC ameliorating the symptoms and/or progression of psoriasis and for
 CC identifying agents useful for treating psoriasis or modulating the
 CC activity of the polypeptide. The polypeptides are also useful for
 CC enhancing the level of CAN-1, STG or SEER-1 biological activity in a cell
 CC or tissue. The nucleic acid molecules are useful as hybridisation probes
 CC in diagnostic procedures (such as diagnosing the presence of psoriasis or
 CC the propensity to develop psoriasis) and for suppressing the expression
 CC of CAN-1 or STG gene (e.g. antisense inhibition, gene therapy).
 CC Antibodies, raised against the polypeptides, are useful for decreasing
 CC the level of CAN-1, STG or SEER-1 biological activity in a cell. The
 CC sequence presented is the human candidate coding sequence-1 (CAN-1) cDNA
 SQ Sequence 891 BP; 169 A; 339 C; 196 G; 187 T; 0 U; 0 Other;

Query Match 100.0%; Score 891; DB 6; Length 891;
 Best Local Similarity 100.0%; Pred. No. 3.9e-225;
 Matches 891; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTCTTGGGGGTTCCAGGACCCAGACTCCAGCCCACTTTGGGGGCCAGTACATA 60
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 QY 61 GCCATGATCTCAACTGGAAGCTCTGGGGATCTGTGCTTGGCTGCACACAGAGGC 120
 Db 61 GCCATGATCTCAACTGGAAGCTCTGGGGATCTGTGCTTGGCTGCACACAGAGGC 120
 QY 121 ATCTCAGGACGAGGAGCCCTCTCACCACCCGACAGAGACCGAGAGGCGAGGC 180
 Db 121 ATCTCAGGACGAGGAGCCCTCTCACCACCCGACAGAGACCGAGAGGCGAGGC 180
 QY 181 TCCCAACATTTGCTCAGGGCCCCCAGTCCCGGTGACCTTGGCAGGGGACCCCT 240
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 QY 241 CTCTTTAAATCTCTCGCTTACCCGCGCCAGTGTCTCTGAGAGACCTGCTGAACCT 300
 Db 241 CTCTTTAAATCTCTCGCTTACCCGCGCCAGTGTCTCTGAGAGACCTGCTGAACCT 300
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 Db 301 GGAATCTGGCCCTGAAACCGCTTAAAGGATCTCTCAACCTCCCGGGCTTACGAC 360
 QY 361 CTTTGGCCGAGAGCCCGACCCCAAGAAACCTCTGGCTCTCTGCTCCCTGAGGTGAC 420
 Db 361 CTTTGGCCGAGAGCCCGACCCCAAGAAACCTCTGGCTCTCTGCTCCCTGAGGTGAC 420
 QY 421 AACGACCTCAGAGAGACCGACCTTACAGCCACCCGGGAAAGAGTACAGATATGAGT 480
 Db 421 AACGACCTCAGAGAGACCGACCTTACAGCCACCCGGGAAAGAGTACAGATATGAGT 480

QY 481 CCCTCAGCCGTTCTGTTCACAGCACTTCAGAGCAACCAGCCCTCTCCACCTCTGAT 540
 Db 481 CCCTCAGCCGTTCTGTTCACAGCACTTCAGAGCAACCAGCCCTCTCCACCTCTGAT 540
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 Db 721 CTCAGGCTCGAGCCCGACCTTACCTCCACCCGGTCTTCTGCGCGGATCGCTGGG 780
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 Db 781 CAGGCTATGTGATCTGTGTCTCTCTCTGCACTGAGTGGCGGACAGAACTATCAAT 840
 QY 841 AGACAGCTGCTGCTTCCATGAAGCGAAATTAATTAATTTCTTTCTTA 891
 Db 841 AGACAGCTGCTGCTTCCATGAAGCGAAATTAATTAATTTCTTTCTTA 891

RESULT 2

ABN60006
 ID ABN60006 standard; cDNA; 1473 BP.

AC ABN60006;

DT 28-UTN-2002 (first entry)

DE Novel human coding sequence SEQ ID NO: 417.

XX Human; anti-neuritic; vulnary; anti-inflammatory; immunomodulator;

KW anti-fertility; cerebroprotective; cytoskeletal; rheumatic; gene therapy;

KW neuroprotective; antiparkinsonian; protein therapy; EST;

XX expressed sequence tag; gene; ss.

OS Homo sapiens.

PN WO200222660-A2.

PD 21-MAR-2002.

PF 10-SEP-2001; 2001WO-US026015.

PR 11-SEP-2000; 2000US-00659671.

PA (HYSE-) HYSEQ INC.

PI Tang YF, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA, Ren F;

PI Xue AJ, Yang Y, Wehrman T, Drmanac RT;

PT MPI; 2002-292406/33.

PS P-PSDB; ABB97593.

XX An isolated polynucleotide for treating diseases associated with its

CC encoded polypeptide such as cancer and multiple sclerosis.

CC Claim 1; SEQ ID NO 417; 509pp; English.

CC The present invention provides the protein and coding sequences of 444

CC novel human proteins. These were isolated from expressed sequences tags

CC (ESTs). They can be used to stimulate cell growth, to regulate

CC haematopoiesis e.g. to treat aplastic anaemia, to help tissue regrowth

CC e.g. in burn treatment, to regulate the immune system e.g. to treat

multiple sclerosis, to regulate activin or inhibin e.g. to treat
CC infertility, to regulate haemostasis or thrombolysis e.g. to treat stroke
CC and cancer, to screen for drugs, to treat inflammatory conditions e.g.
CC rheumatoid arthritis, and to treat nervous system disorders e.g.
CC Parkinson's disease. The present sequence is a coding sequence of the
CC invention

XX Sequence 1473 BP; 294 A; 491 C; 382 G; 306 T; 0 U; 0 Other;

Query Match 99.5%; Score 886.2; DB 6; Length 1473;
Best Local Similarity 99.7%; Pred. No. 8.7e-224;
Matches 888; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db 633 GCCATGATCTCACTGAAGCTCTGGGGATCTGGTCTTTGCTTGCAACACAGAGGC 692
QY 121 ATCTCAGGACGCGAGGGCCACCCCTCTCACCCACCCGACAGAGACCGAGAGAGGACGAC 180
Db 693 ATCTCAGGACGCGAGGGCCACCCCTCTCACCCACCCGACAGAGACCGAGAGAGGACGAC 752
QY 181 TCCCAACATTTGCTCAGGGGCCCCAGTCCCGGGTGAACCTTGCGCCAGAGGACCCCT 240
Db 753 TCCCAACATTTGCTCAGGGGCCCCAGTCCCGGGTGAACCTTGCGCCAGAGGACCCCT 812
QY 241 CTCTTTGAAGATCTCTCCGCTACCCGCCAGTGTCTCTGAGAGACCTGCTGAACCT 300
Db 813 CTCTTTGAAGATCTCTCCGCTACCCGCCAGTGTCTCTGAGAGACCTGCTGAACCT 872
QY 301 GAGATCTGGGCCCCCTGAAACCGGCTTGAAGAGATCTCTCTCAACTCCCGGCTGACGAC 360
Db 873 GAGATCTGGGCCCCCTGAAACCGGCTTGAAGAGATCTCTCTCAACTCCCGGCTGACGAC 932
QY 361 CTTTGGCGGAGGACCCCAAGAACCCCTGAGCTCTTGCCCTGAGGAGTGAAC 420
Db 933 CTTTGGCGGAGGACCCCAAGAACCCCTGAGCTCTTGCCCTGAGGAGTGAAC 992
QY 421 AACGACCTCAGAGAGAGCCAGACTTGAACCCACCCGGAGAGATACAGATTAATGAGT 480
Db 993 AACGACCTCAGAGAGAGCCAGACTTGAACCCACCCGGAGAGATACAGATTAATGAGT 1052
QY 481 CCGCTCAGCGGTTGTCTCCAGGATCTCAGGACCCAGCCCTCTCAACCTCTGAT 540
Db 1053 CCGCTCAGCGGTTGTCTCCAGGATCTCAGGACCCAGCCCTCTCAACCTCTGAT 1112
QY 541 TCCCGGGAATTTCTCCCAATTTAGCTATCTCTTAAACCTCTTCCATTCCTCGGT 600
Db 1113 TCCCGGGAATTTCTCCCAATTTAGCTATCTCTTAAACCTCTTCCATTCCTCGGT 1172
QY 601 TTTATTTGAAACCCGTAAGGTGTCTCAATATTTCTGTCTCCCTCTGAGATCCATA 660
Db 1173 TTTATTTGAAACCCGTAAGGTGTCTCAATATTTCTGTCTCCCTCTGAGATCCATA 1232
QY 661 CTTAGTCTTCAATGCGCCGTTTTTTTCTCTGACAGCTTAAAGCTTACTCTCTACCTGCG 720
Db 1233 CTTAGTCTTCAATGCGCCGTTTTTTTCTCTGACAGCTTAAAGCTTACTCTCTACCTGCG 1292
QY 721 CTCGAGGCTTCGAGCCCACTACCTCCACCCCGGCTTTCGCGCCGAGATGCTGGGG 780
Db 1293 CTCGAGGCTTCGAGCCCACTACCTCCACCCCGGCTTTCGCGCCGAGATGCTGGGG 1352
QY 781 CAGGGCTATGGTACTGTGTTCCTTCTGCAACTGTGTGCGCGGAGGAGAACTATCAGT 840
Db 1353 CAGGGCTATGGTACTGTGTTCCTTCTGCAACTGTGTGCGCGGAGGAGAACTATCAGT 1412
QY 841 AGACAGCTGCTGCTTCCATGAAACGGAATAAATCATGTTTCTTAA 891
Db 1413 AGACAGCTGCTGCTTCCATGAAACGGAATAAATCATGTTTCTTAA 1463
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RESULT 3
ID ABR66967 standard; DNA: 2997 BP.
XX
AC ABR66967,
XX
DT 24-SEP-2002 (first entry)
XX
DE Human CAN-1 deletion polymorphism genomic DNA.
XX
XX Human; antipsoriatic; chromosome 6; candidate coding sequence-1; CAN-1;
XX SEER-1; STG; human leukocyte antigen C; HLA C; HLA Cw6; psoriasis; skin;
XX keratinocyte; chronic inflammatory dermatosis; erythroderma; seboreic;
XX guttate; pustular variant; Reiter's disease; hyperproliferation;
XX epidermis; differentiation; diagnosis; gene therapy; gene; ds; SNP;
XX single nucleotide polymorphism; deletion polymorphism.
XX
OS Homo sapiens.
XX
FH Key
FT variation
FT Location/Qualifiers
FT /tag= a
FT /note= "Deletion polymorphism"
FT replaces(114,T)
FT /tag= b
FT /strand name= "Single nucleotide polymorphism"
FT replace(361,A)
FT
FT /tag= c
FT /strand name= "Single nucleotide polymorphism"
FT replace(550,A)
FT /tag= d
FT /strand name= "Single nucleotide polymorphism"
FT replace(966,G)
FT /tag= e
FT /strand name= "Single nucleotide polymorphism"
FT replace(1096,T)
FT /tag= f
FT /strand name= "Single nucleotide polymorphism"
FT replace(1196,A)
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FT /tag= g
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FT /product= "CAN-1"
FT 1461..1535
FT /tag= j
FT /number= 1
FT 1536..2201
FT /tag= k
FT /number= 1
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FT /tag= l
FT /strand name= "Single nucleotide polymorphism"
FT replace(1875,T)
FT /tag= m
FT /strand name= "Single nucleotide polymorphism"
FT replace(1982,A)
FT /tag= n
FT /strand name= "Single nucleotide polymorphism"
FT replace(2016,C)
FT /tag= o
FT /strand name= "Single nucleotide polymorphism"
FT replace(2107,G)
FT /tag= p
FT /strand name= "Single nucleotide polymorphism"
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FT /tag= q
FT /number= 2
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FT variation
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FT      /*tag= s
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FT      /replace(2618,G)
FT      /*tag= t
FT      /standard_name= "Single nucleotide polymorphism"
FT      /replace(2671,C)
FT      /*tag= u
FT      /standard_name= "Single nucleotide polymorphism"
PN      W0200244375-A2.
XX      06-JUN-2002.
XX      27-NOV-2001; 2001WO-US044506.
XX      28-NOV-2000; 2000US-0253592P.
XX      PR 15-DEC-2000; 2000US-0256839P.
XX      (CELL-) CELTECH R & D INC.
XX      Charmley P, Moss P, Mceuen M;
XX      WPI; 2002-508513/54.
XX      P-PSDB; AAU79579.
XX      Novel isolated CAN-1 polypeptide involved in keratinocyte proliferation
XX      PT and differentiation, and polynucleotides encoding the polypeptide, useful
XX      for diagnosing or predicting susceptibility to psoriasis in individual.
XX      Example 3; Page 92-93; 95pp; English.
XX      The invention discloses isolated candidate coding sequence-1 (CAN-1),
XX      CC SEEK-1 (not defined) and STG (not defined) polypeptides, and the
XX      CC polynucleotides encoding them. All three genes were identified due to
XX      CC their proximity to the human leukocyte antigen C (HLA C) locus on
XX      CC chromosome 6. The HLA Cw6 allele is associated with psoriasis and as the
XX      CC three genes are expressed in normal skin and/or keratinocyte tissue, the
XX      CC may also have a role in psoriasis. Psoriasis is a chronic inflammatory
XX      CC dermatosis that is characterised by hyperproliferation of epidermal
XX      CC cells. Possible treatments against psoriasis involve the inhibition of
XX      CC movement of cells into the epidermis, or the inhibition of
XX      CC hyperproliferation or abnormal differentiation of keratinocytes, by the
XX      CC inhibition of the CAN-1, STG or SEEK-1 polypeptides binding to their
XX      CC binding partners. The polypeptides are useful for diagnosing or
XX      CC predicting the susceptibility to psoriasis in an individual, for
XX      CC ameliorating the symptoms and/or progression of psoriasis and for
XX      CC identifying agents useful for treating psoriasis or modulating the
XX      CC activity of the polypeptide. The polypeptides are also useful for
XX      CC enhancing the level of CAN-1, STG or SEEK-1 biological activity in a cell
XX      CC or tissue. The nucleic acid molecules are useful as hybridisation probes
XX      CC in diagnostic procedures (such as diagnosing the presence of psoriasis or
XX      CC the propensity to develop psoriasis) and for suppressing the expression
XX      CC of CAN-1 or STG gene (e.g. antisense inhibition, gene therapy).
XX      CC Antibodies, raised against the polypeptides, are useful for decreasing
XX      CC the level of CAN-1, STG or SEEK-1 biological activity in a cell. The
XX      CC sequence presented is the human candidate coding sequence-1 (CAN-1)
XX      CC deletion polymorphism genomic DNA
XX      SQ Sequence 2997 BP; 617 A; 785 C; 913 G; 682 T; 0 U; 0 Other;
XX      Query Match      87.0%; Score 775.4; DB 6; Length 2997;
XX      Best Local Similarity 99.9%; Pred. No. 2,1e-194;
XX      Matches 776; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY      115 AGAGGATCTTCAGGACGAGGAGCCCTCTTACCCACCCGAGAGAGAGAGAG 174
DB      2198 ACAGGATCTTCAGGACGAGGAGCCCTCTTACCCACCCGAGAGAGAGAG 2257
QY      175 GCAAGCTCCCCAATTCCTCAGGAGCCCGCCGATACCTTGGCAGAGGCA 234

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DB      2258 GCAAGCTCCCCAATTCCTCAGGAGCCCGCCGATACCTTGGCAGAGGCA 2317
QY      235 CCCCCTCTTTGAAGATCTCCGCTACCGGCGCCAGTGCTCCGAGAGACTGCTT 294
DB      2318 CCCCCTCTTTGAAGATCTCCGCTACCGGCGCCAGTGCTCCGAGAGACTGCTT 2377
QY      295 GAAACTGAGTCTGGCCCGCTGAGACCGCTGAGAGGATCTTCAACTCCCGGCT 354
DB      2378 GAAACTGAGTCTGGCCCGCTGAGACCGCTGAGAGGATCTTCAACTCCCGGCT 2437
QY      355 GACGACCTTGGCCCGGAGAGACCCGAGAGGAGGAGGAGGAGGAGGAGGAG 414
DB      2438 GACGACCTTGGCCCGGAGAGACCCGAGAGGAGGAGGAGGAGGAGGAGGAG 2497
QY      415 GTGAGACACCGACTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATA 474
DB      2498 GTGAGACACCGACTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATA 2557
QY      475 TGAGATCCCTCAGCCGTTCTGTTCCAGGAGATCTCCAGGACCAAGCCCTTCCACC 534
DB      2558 TGAGATCCCTCAGCCGTTCTGTTCCAGGAGATCTCCAGGACCAAGCCCTTCCACC 2617
QY      535 TCTGATTTCCCGTGAATCTTCTCCCAATTAAGCTATCTCTTAACCTCTTCAATTC 594
DB      2618 TCTGATTTCCCGTGAATCTTCTCCCAATTAAGCTATCTCTTAACCTCTTCAATTC 2677
QY      595 CTCGGTTTATTTGAAACCGTAAAGGTGTTGTTCTCAATATTTCTGTCCTCCCTGAGA 654
DB      2678 CTCGGTTTATTTGAAACCGTAAAGGTGTTGTTCTCAATATTTCTGTCCTCCCTGAGA 2737
QY      655 TCCATATTAATGCTCAATGCGCGTTTCTTCTGACAGCTTAAAGCTACTCTCTTA 714
DB      2738 TCCATATTAATGCTCAATGCGCGTTTCTTCTGACAGCTTAAAGCTACTCTCTTA 2797
QY      715 CTCGGCTCCAGGAGCCCTGCGCCCACTACTCTCCACCGGCTTCTGCGCCGAGATG 774
DB      2798 CTCGGCTCCAGGAGCCCTGCGCCCACTACTCTCCACCGGCTTCTGCGCCGAGATG 2857
QY      775 CTCGGGACAGGAGCTATGTAATGTTCCCTTCTGACCTGAGTGGCGGAGAGACT 834
DB      2858 CTCGGGACAGGAGCTATGTAATGTTCCCTTCTGACCTGAGTGGCGGAGAGACT 2917
QY      835 ATCAGTAGACAGTGTCTGCTTCCATGAAACGAAATTAATCATGTTTCTTAA 891
DB      2918 ATCAGTAGACAGTGTCTGCTTCCATGAAACGAAATTAATCATGTTTCTTAA 2974
RESULT 4
ABK86963
ID      ABK86963 standard; DNA; 3001 BP.
XX      AC      ABK86963;
XX      DT      24-SEP-2002 (first entry)
XX      DE      Human candidate coding sequence-1 (CAN-1) genomic DNA.
XX      KW      Human; antipsoriatic; chromosome 6; candidate coding sequence-1; CAN-1;
XX      KW      SEEK-1; STG; human leukocyte antigen C; HLA C; HLA Cw6; psoriasis; skin;
XX      KW      keratinocyte; chronic inflammatory dermatosis; erythroderma; seborrheic;
XX      KW      guttate; pustular variant; Reiter's disease; hyperproliferation;
XX      KW      epidermis; differentiation; diagnosis; gene therapy; gene; ds; SNP;
XX      KW      single nucleotide polymorphism; deletion polymorphism.
XX      OS      Homo sapiens.
XX      FH      Key
XX      FT      variation
XX      FT      Location/Qualifiers
XX      FT      /tag= a
XX      FT      /note= "Deletion polymorphism"
XX      FT      /replace(118,T)
XX      FT      /*tag= b
XX      FT      /standard_name= "Single nucleotide polymorphism"

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FT      /standard_name= "Single nucleotide polymorphism"
FT      replace(1100,T)
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FT      replace(1394,T)
FT      /*tag= f
FT      /standard_name= "Single nucleotide polymorphism"
FT      CDS
FT      1485..2561
FT      /*tag= g
FT      /product= "CAN-1"
FT      1485..1539
FT      /*tag= h
FT      /number= 1
FT      intron
FT      1540..2205
FT      /*tag= i
FT      /number= 1
FT      variation
FT      replace(1681,A)
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FT      replace(1879,T)
FT      /*tag= k
FT      /standard_name= "Single nucleotide polymorphism"
FT      replace(1986,A)
FT      /*tag= l
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FT      /*tag= n
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FT      exon
FT      2206..2561
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FT      MO200244375-A2.
FT      PN
FT      PD
FT      06-JUN-2002.
FT      XX
FT      27-NOV-2001; 2001WO-US044506.
FT      XX
FT      28-NOV-2000; 2000US-0253592P.
FT      PR
FT      15-DEC-2000; 2000US-0256839P.
FT      XX
FT      PA
FT      (CELL-) CELUTECH R & D INC.
FT      PI
FT      Charmley P, Moss P, Mceuen M;
FT      XX
FT      DR
FT      MPI; 2002-508513/54.
FT      DR
FT      P-PSDB; AAU79579.
FT      XX
FT      Novel, isolated CAN-1 polypeptide involved in keratinocyte proliferation
FT      and differentiation, and polynucleotides encoding the polypeptide, useful
FT      for diagnosing or predicting susceptibility to psoriasis in individual.
FT      PS
FT      Claim 18; Page 82-84; 95pp; English.
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XX      The invention discloses isolated candidate coding sequence-1 (CAN-1),
CC      SEEK-1 (not defined) and STG (not defined) polypeptides, and the
CC      polynucleotides encoding them. All three genes were identified due to
CC      their proximity to the human leukocyte antigen C (HLA C) locus on
CC      chromosome 6. The HLA Cw6 allele is associated with psoriasis and as the
CC      three genes are expressed in normal skin and/or keratinocyte tissue, they
CC      may also have a role in psoriasis. Psoriasis is a chronic inflammatory
CC      dermatosis that is characterised by hyperproliferation of epidermal
CC      cells. Possible treatments against psoriasis involve the inhibition of
CC      movement of cells into the epidermis, or the inhibition of
CC      hyperproliferation or abnormal differentiation of keratinocytes, by the
CC      inhibition of the CAN-1, STG or SEEK-1 polypeptides binding to their
CC      binding partners. The polypeptides are useful for diagnosing or
CC      predicting the susceptibility to psoriasis in an individual, for
CC      ameliorating the symptoms and/or progression of psoriasis and for
CC      identifying agents useful for treating psoriasis or modulating the
CC      activity of the polypeptide. The polypeptides are also useful for
CC      enhancing the level of CAN-1, STG or SEEK-1 biological activity in a cell
CC      or tissue. The nucleic acid molecules are useful as hybridisation probes
CC      in diagnostic procedures (such as diagnosing the presence of psoriasis or
CC      the propensity to develop psoriasis) and for suppressing the expression
CC      of CAN-1 or STG gene (e.g. antisense inhibition, gene therapy).
CC      Antibodies, raised against the polypeptides, are useful for decreasing
CC      the level of CAN-1, STG or SEEK-1 biological activity in a cell. The
CC      sequence presented is the human candidate coding sequence-1 (CAN-1)
CC      genomic DNA
XX
XX      Sequence 3001 BP; 619 A; 786 C; 914 G; 682 T; 0 U; 0 Other;
SQ
Query Match      87.0%; Score 775.4; DB 6; Length 3001;
Best Local Similarity 99.9%; Pred. No. 2,1e-194;
Matches 776; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY      115 AGAGGCAATCTCAGGACGAGGACGACCCCTCTCACCACCCGAGAGACCGAGAGAG 174
DB      2202 ACAGGCAATCTCAGGACGAGGACGACCCCTCTCACCACCCGAGAGACCGAGAGAG 2261
QY      175 GCAGGCTCCCAATGCTCCTCAGGAGCCCGCCAGTCCCGGTGACCTTGCGGCGAGGCA 234
DB      2262 GCAGGCTCCCAATGCTCCTCAGGAGCCCGCCAGTCCCGGTGACCTTGCGGCGAGGCA 2321
QY      235 CCCCCTCTTTGAGAGATCTCCGCTACCCGCGCCAGTGCCTCTGAGAGACTCTCT 294
DB      2322 CCCCCTCTTTGAGAGATCTCCGCTACCCGCGCCAGTGCCTCTGAGAGACTCTCT 2381
QY      295 GAAACTGAGATCTGAGCCCTCTGAAACGCGCTGAAACGAGATCTCTCAACTCTCCCGGCT 354
DB      2382 GAAACTGAGATCTGAGCCCTCTGAAACGCGCTGAAACGAGATCTCTCAACTCTCCCGGCT 2441
QY      355 GACGACCTTGGCCGCGAGAGACCCAGCCCGCCAGAAACCCCTGCGCCCTGAG 414
DB      2442 GACGACCTTGGCCGCGAGAGACCCAGCCCGCCAGAAACCCCTGCGCCCTGAG 2501
QY      415 GTGACACACGACCTCAGAGAGACGACCTAGACCCAGCCCGGAGAGAGATGATTA 474
DB      2502 GTGACACACGACCTCAGAGAGACGACCTAGACCCAGCCCGGAGAGAGATGATTA 2561
QY      475 TGAAGTCCCTCAGCGGTCTGTTCCAGGACATCTCAGGACCCAGCCCTCTCCACC 534
DB      2562 TGAAGTCCCTCAGCGGTCTGTTCCAGGACATCTCAGGACCCAGCCCTCTCCACC 2621
QY      535 TGTGATTCCTCCGAGATTTCTCCCAATTGACCTATCTCTTAACCTCTTCTCATTC 594
DB      2622 TGTGATTCCTCCGAGATTTCTCCCAATTGACCTATCTCTTAACCTCTTCTCATTC 2681
QY      595 CTGGTTTATCTGAAACCGGTAGGTGTTCTCAATATTTCTGCTCCCTCTGAGA 654
DB      2682 CTGGTTTATCTGAAACCGGTAGGTGTTCTCAATATTTCTGCTCCCTCTGAGA 2741
QY      655 TCATACTAGTCTCAGATGCGCGTTTCTCTGACAGCTAAGCTACTCTCTTA 714
DB      2742 TCATACTAGTCTCAGATGCGCGTTTCTCTGACAGCTAAGCTACTCTCTTA 2801
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QY 715 CTGCGCTCCAGAGGCTCGGCCCCCACTACTCCACCGGGTCTTCTGCGCGCGAGATCG 774
 DB 2802 CCTGCGCTCCAGAGGCTCGGCCCCCACTACTCCACCGGGTCTTCTGCGCGCGAGATCG 2861
 QY 775 CTGCGCGAGGCTATGTAAGTGTGTGCTTCTGCGCATGCTGCGCGCGAGAACT 834
 DB 2862 CTGCGCGAGGCTATGTAAGTGTGTGCTTCTGCGCATGCTGCGCGCGAGAACT 2921
 QY 835 ATCAGTAGACAGCTGCTGCTTCCATGAACGAAAAAATCAATGTTTCTTAA 891
 DB 2922 ATCAGTAGACAGCTGCTGCTTCCATGAACGAAAAAATCAATGTTTCTTAA 2978

RESULT 5
 AB075680
 ID AB075680 standard; DNA; 55050 BP.
 AC AB075680;
 XX 11-NOV-2002 (first entry)
 DT 11-NOV-2002 (first entry)
 XX Human SEBK1 consensus genomic DNA.
 DE Human; SEBK1; chromosome 6p21; inflammatory disease; antiinflammatory;
 KM antiporiatic; gene therapy; gene; ds.
 KW Homo sapiens.
 OS WO200264831-A2.
 XX 22-AUG-2002.
 PD 13-FEB-2002; 2002WO-GB000653.
 XX 13-FEB-2001; 2001GB-00003514.
 PR (OXAG-) OXAGEN LTD.
 PA Lench NJ, Allen MJ, Nicholls RK,
 PI WPI; 2002-667013/71.
 DR PT Polymorphisms in the SEBK1 gene and polynucleotides encoding the SEBK1
 PT gene, for treating, diagnosing or determining susceptibility to SEBK1
 PT mediated disease, e.g. inflammatory disease such as psoriasis.
 XX Claim 4; Fig 2; 69pp; English.
 PS The present invention describes a polynucleotide (I) comprising: (a) a
 CC nucleic acid sequence (II) encoding the SEBK1 gene; (b) a nucleic acid
 CC sequence (III) encoding a fragment of the SEBK1 gene; or (c) a nucleic
 CC acid sequence (IV) that hybridises under stringent conditions to the
 CC polynucleotide of (II) or (III). (I) has antiinflammatory and
 CC antiporiatic activities and can be used in gene therapy. The alleles of
 CC one or more polymorphisms in the SEBK1 gene can be used for the
 CC manufacture of a medicament for the diagnosis and treatment of SEBK1
 CC mediated disease. SEBK1 protein fragments are useful in diagnostic,
 CC prognostic or therapeutic methods, or as research tools in drug
 CC screening. Human SEBK1 is located to chromosome 6p21. The present
 CC sequence represents a human SEBK1 nucleotide sequence
 CC XX

Sequence 55050 BP; 13076 A; 14198 C; 14560 G; 13197 T; 0 U; 19 Other;
 Query Match 87.0%; Score 775; DB 6; Length 55050;
 Best Local Similarity 99.7%; Pred. No. 7e-194;
 Matches 775; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 115 AGAGGCTCTCCAGGCGAGGCGCACCTCTTCCACCCGAGAGAGAGAGAG 174
 DB 27096 AGAGGCTCTCCAGGCGAGGCGCACCTCTTCCACCCGAGAGAGAGAG 27155
 QY 175 GCAGGCTCCCAACATTTGCTCAAGGCGCCCCCAGTCCCGGTACCTTTGCCAGGGCA 234

DB 27156 GCAGGCTCCCAACATTTGCTCAAGGCGCCCCCAGTCCCGGTACCTTTGCCAGGGCA 27215
 QY 235 CCCCCTCTTTTGAAGATCTCCGCTTACCGGCCCACTGCTCTTGGAGAGAGCTGCTT 294
 DB 27216 CCCCCTCTTTTGAAGATCTCCGCTTACCGGCCCACTGCTCTTGGAGAGAGCTGCTT 27275
 QY 295 GAAATCGAATCTGGCCCCCTGAAACCGGCTTGAAGAGATCTCTCAACTCCCGGCTT 354
 DB 27276 GAAATCGAATCTGGCCCCCTGAAACCGGCTTGAAGAGATCTCTCAACTCCCGGCTT 27335
 QY 355 GACGACCTTTGGCCGCGAGAGACCCCAAGCCCAAGAAACCTCTGAGCTCTGAG 414
 DB 27336 GACGACCTTTGGCCGCGAGAGACCCCAAGCCCAAGAAACCTCTGAGCTCTGAG 27395
 QY 415 GTGAGACACCGAGCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATTA 474
 DB 27396 GTGAGACACCGAGCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATTA 27455
 QY 475 TGGAGTCCCTCAGCCGTTCTGTTCCAGGAGATCTCAGGAGAGAGAGAGAGAGAG 534
 DB 27456 TGGAGTCCCTCAGCCGTTCTGTTCCAGGAGATCTCAGGAGAGAGAGAGAGAG 27515
 QY 535 TGTGATTCCTCGGAGATTTCTCCAAATTAAGCTTATCTCTTAACTCTTCTCATTC 594
 DB 27516 TGTGATTCCTCGGAGATTTCTCCAAATTAAGCTTATCTCTTAACTCTTCTCATTC 27575
 QY 595 CTGCGTTTATCTGAAACCGTGAAGGTGATCTCAATTTCTCTGCTCCCTCCAGAA 654
 DB 27576 CTGCGTTTATCTGAAACCGTGAAGGTGATCTCAATTTCTCTGCTCCCTCCAGAA 27635
 QY 655 TCCATCTTAGTCTCAGATCGCCGTTTCTCTGACAGGCTTAAAGCTTACTCTTA 714
 DB 27636 TCCATCTTAGTCTCAGATCGCCGTTTCTCTGACAGGCTTAAAGCTTACTCTTA 27695
 QY 715 CTTGCGCTCAGAGCTCTGAGCCCACTTACCTCCACCCGCTTCTCTGCGCGAGTCG 774
 DB 27696 CTTGCGCTCAGAGCTCTGAGCCCACTTACCTCCACCCGCTTCTCTGCGCGAGTCG 27755
 QY 775 CTGCGGAGGCGATGTAAGTGTGTGCTTCTGCGCATGCTGAGCGCGGAGAGAACT 834
 DB 27756 CTGCGGAGGCGATGTAAGTGTGTGCTTCTGCGCATGCTGAGCGCGGAGAGAACT 27815
 QY 835 ATCAGTAGACAGCTGCTGCTTCCATGAACGAAAAAATCAATGTTTCTTAA 891
 DB 27816 ATCAGTAGACAGCTGCTGCTTCCATGAACGAAAAAATCAATGTTTCTTAA 27872

RESULT 6
 AAH45310
 ID AAH45310 standard; DNA; 25235 BP.
 XX AAH45310,
 AC AAH45310,
 XX 01-OCT-2001 (first entry)
 DT 01-OCT-2001 (first entry)
 XX Human SEBK1 DNA.
 DE Human; MHC S; major histocompatibility complex S; vulgar psoriasis;
 KM diagnosis; primer; SEBK1; HCR; a-helix coiled-coil rod homologue;
 KW polymorphism; ds.
 XX Homo sapiens.
 OS Homo sapiens.
 XX

Key Location/Qualifiers
 FT exon 1..420
 FT /*tag= a
 FT 421..1281
 FT /*tag= b
 FT exon 1282..1405
 FT /*tag= c
 FT 1406..1601
 FT /*tag= d

FT	exon		/tag=	e	1602.	.1702
FT	intron		/tag=	f	1703..	.2351
FT	exon		/tag=	g	2352..	.2364
FT	intron		/tag=	h	2365..	.6286
FT	exon		/tag=	i	6287..	.6509
FT	intron		/tag=	j	6510..	.10416
FT	exon		/tag=	k	10417..	.10493
FT	intron		/tag=	l	10494..	.14243
FT	exon		/tag=	m	14244..	.14407
FT	intron		/tag=	n	14408..	.14243
FT	exon		/tag=	o	25190..	.25235
PD	MOZ00142458-AL.					
PD	14-JUN-2001.					
PP	06-DEC-2000; 2000MO-JP008624.					
PR	06-DEC-1999; 99JP-00346867.					
PA	(INOK/) INOKO H.					
PI	Inoko H., Tamiya G;					
DR	WPI, 2001-381680/40.					
PT	New primer DNA, useful for detecting vulgar psoriasis.					
PS	Claim 1; Page 46-62; 106pp; Japanese.					
XX	The invention relates to a method of diagnosing vulgar psoriasis using primers based on the sequences of the human MHC S, SEBXI and HCR genes.					
CC	By analysing the sequences of these genes in Japanese patients with psoriasis and in normal subjects, it has been found that some of the examined polymorphisms correlate significantly to the group of patients with psoriasis. Vulgar psoriasis can therefore be diagnosed by analysing these gene polymorphisms. The present sequence is the human SEBXI gene which was used to design primers for use in the invention					
SQ	Sequence 25235 BP; 5967 A; 6703 C; 6487 G; 6078 T; 0 U; 0 Other;					
Query Match	86.8%; Score 773.8; DB 4; Length 25235;					
Beet Local Similarity	99.7%; Pred. No. 1.1e-193;					
Matches	775; Conservative 0; Mismatches 2; Indels 0; Gaps 0;					
Dy	115 AGAGGCAATCTGAAGCAGCGAAGGGCACCCCTTACACCACCGCAGAAGAACGAGAG 174					
Dd	1751 ACAGGCATCTCAGGCAAGGAGGGCCAACCTCTTCACCAACCGCAGAAGACTCGAAGAG 1810					
Df	175 GCAGGCTCCCCAAATTGTCTTGAGGCCCCCACAAGTCCCGGTGACCTTTGGCCAGGGGCA 234					
Dg	1811 GCAGGCTCCCCAAATTGTCTTGAGGCCCCCACAAGTCCCGGTGACCTTTGGCCAGGGGCA 1870					
Dh	235 CCCCTCTCTTTGAAGATCTCCGCTACCCGCCCATCGTCCCTGGAGAGACTGCT 294					
Di	1871 CCCTCTCTTTGAAGATCTCCGCTACCCGCCCATCGTCCCTGGAGAGACTGCT 1930					
Dj	295 GAACCTGAGTCTGGCCCCCTTAACCGGCTTAGAGAGATCTCTCAAATCTCCCGGCT 354					
Dk	1931 GAACCTGAGTCTGGCCCCCTTAACCGGCTTAGAGAGATCTCTCAAATCTCCCGGCT 1990					
DL	355 GACGACCTTGAGCTGGCGGAGAACCCGAGCCCCCAGAAAACCCCTGGCTCTGCCCCTAG 414					

Db	1991	GACGACCCCTTGGCCGCGCAGAGACCCAGCCCCAGAAAAACCCCTGGCTCTGCCCCCTGAG	2050
Qy	415	GTGAGCAACCGACCTCAGAGAGAGCCAGACCTAGACCCACCCGCGGAAAGAGTACAGATTA	474
Db	2051	GTGAGCAACCGACCTCAGAGAGAGCAGACCTAGACCCACCCCGGAAAGAGTACAGATTA	2110
Qy	475	TGGAATCCCCCTCAGCCGCTTCTGTTCCTCAGGCACTCTCCAGGACCCAGCCCTCTCCACC	534
Db	2111	TGGAATCCCCCTCAGCCGCTTCTGTTCCTCAGGCACTCTCCAGGACCCAGCCCTCTCCACC	2170
Qy	535	TCTGATCCCCGATGATCTTCCCAATTAGCCATGCTCTTAAACCTCTTCAATCC	594
Db	2111	TCTGATCCCCGATGATCTTCCCAATTAGCCATGCTCTTAAACCTCTTCAATCC	2230
Qy	595	CTCGGTTTATTTCTGAAACCCGTAAGGATGATGTTCTCAATATTTCCCTGCTCCAGGA	654
Db	2231	CTCGGTTTATTTCTGAAACCCGTAAGGATGATGTTCTCAATATTTCCCTGCTCCAGGA	2290
Qy	655	TCCATACTTAAAGTCCCTCAGTCAGCCCGCTTTTCTCTGACAGCCTAAGCCTACTCTCCTA	714
Db	2291	TCCATACTTAAAGTCCCTCAGTCAGCCCGCTTTTCTCTGACAGCCTAAGCCTACTCTCCTA	2350
Qy	715	CCTGSCCTCAGGCTCTGSCCCCAACCTACCTCCACCCGCTCTCTGSCCGCGAGATCG	774
Db	2351	CCTGSCCTCAGGCTCTGSCCCCAACCTACCTCCACCCGCTCTCTGSCCGCGAGATCG	2410
Qy	775	CTGGGGCAGGGCTATAGTACTGTGTCCCTTCTGCACTGTGAGCGGCGGAGAGAACT	834
Db	2411	CTGGGGCAGGGCTATAGTACTGTGTCCCTTCTGCACTGTGAGCGGCGGAGAGAACT	2470
Qy	835	ATCAGTAGACAGCTGCTGCTTCCATGAACGAAAAATATAAATCATGTTTCTTTAA	891
Db	2471	ATCAGTAGACAGCTGCTGCTTCCATGAACGAAAAATATAAATCATGTTTCTTTAA	2527
RESULT 7			
ACH72505			
ID	ACH72505	standard; DNA; 565 BP.	
XX	ACH72505;		
AC	29-JUL-2004	(first entry)	
XX			
DT			
XX			
DE		Human genome derived single exon probe #5700.	
XX			
KM		Human; probe; ss; gene expression; single exon probe; microarray;	
XX		alternative splicing event; genomic alteration.	
OS		Homo sapiens.	
XX			
PN		US2003194704-A1.	
XX			
PD		16-OCT-2003.	
XX			
PF		03-APR-2002; 2002US-00029386.	
XX			
PR		03-APR-2002; 2002US-00029386.	
XX			
PA		(PENNY/) PENN S G.	
XX		(RANK/) RANK D R.	
PA		(HANZ/) HANZEL D K.	
XX			
PI		Penn SG, Rank DR, Hanzel DK;	
XX			
DR		WPI; 2004-119264/12.	
XX			
PT		New human genome-derived single exon nucleic acid probes useful for human	
XX		gene expression analysis, for identifying or characterizing alternative	
PT		splicing events, for assessing genomic alterations or as tools for	
XX		surveying tissues.	
PS		Claim 15; SEQ ID NO 5700; 80bp; English.	

XX The invention relates to a nucleic acid probe for measuring human gene expression, comprising any of the 27,400 fully defined nucleotide sequences in the specification, or their complements or fragments, and encoding at least 8 amino acids of any of the 688 amino acid sequences fully defined in the specification. The probe is a single exon probe that hybridises under high stringency conditions to a nucleic acid molecule expressed in human cells or tissues. Also included are a spatially-addressable set of single exon nucleic acid probes for measuring human gene expression (comprising a plurality of single exon nucleic acid probes cited above, where each of the plurality of probes is separately and addressably isolatable or amplifiable from the plurality), a single exon microarray for measuring human gene expression, a method of measuring human gene expression, a vector comprising the single exon probe cited above, an ORF-encoded peptide comprising at least 8 contiguous amino acids of any of the above-mentioned amino acid sequences (optionally with conservative amino acid substitutions), an isolated antibody that binds specifically to a peptide cited above, a customer desiring to measure gene expression, a method of providing human gene expression data by subscription, and a computer-readable storage medium which contains a database having a plurality of records (each record including data on the expression of a single exon probe cited above. The probe, methods and apparatus are useful in gene expression analysis. The probes may be used as tools for surveying tissues to detect the presence of expressed messages that contain their specific exon, or in constructing genome-derived single exon microarrays. In addition, the probes are used in identifying and characterising alternative splicing events, in detecting and characterising gross alterations in the genomic locus that includes their exon, in assessing smaller genomic alterations, in priming the synthesis of nucleic acids, or in expressing the ORF-encoded peptide. The present sequence is a human single exon probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html?docID=20030194704

Sequence 565 BP; 99 A; 227 C; 112 G; 127 T; 0 U; 0 Other;

Query Match 63.2%; Score 563.4; DB 12; Length 565;

Best Local Similarity 99.8%; Pred. No. 1.2e-138;

Matches 564; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 235 CCCCCTCTTTGAAGATCTCCGCTACCCGCCAGTGTCTCTGAAGACCTGCT 294
 Db 1 CCCCCTCTTTGAAGATCTCCGCTACCCGCCAGTGTCTCTGAAGACCTGCT 60
 QY 295 GAAACTGAGTCTGGCCCTGAAACCGGCTAGAACGGATCTCTCAACTCCCGGCT 354
 Db 61 GAAACTGAGTCTGGCCCTGAAACCGGCTAGAACGGATCTCTCAACTCCCGGCT 120
 QY 355 GACGACCTTGGCCGCGAGAGACCCAGACCCCGCAGAAAAACCTGTGCTCTGCTGAG 414
 Db 121 GACGACCTTGGCCGCGAGAGACCCAGACCCCGCAGAAAAACCTGTGCTCTGCTGAG 180
 QY 415 GTGAGCAACGCACTCGAGAGAGAGACGACTTGAACCCACCCGCGGAGAGTACAGATA 474
 Db 181 GTGAGCAACGCACTCGAGAGAGAGACGACTTGAACCCACCCGCGGAGAGTACAGATA 240
 QY 475 TGGAGTCCCTCAGCCGCTTCTGTTCCAGGATCTCCAGGACACCGCCCTCCACCC 534
 Db 241 TGGAGTCCCTCAGCCGCTTCTGTTCCAGGATCTCCAGGACACCGCCCTCCACCC 300
 QY 535 TCTGATTCCCGTGAATTTCTTCCAAATTAGCTATCTCTTAAACCTTCTCTCATTC 594
 Db 301 TCTGATTCCCGTGAATTTCTTCCAAATTAGCTATCTCTTAAACCTTCTCTCATTC 360
 QY 595 CTGGGTTTATCTGGAACCCGTAAGGTGTCTCAATTTCTCTGCTCCCTCTGAGA 654
 Db 361 CTGGGTTTATCTGGAACCCGTAAGGTGTCTCAATTTCTCTGCTCCCTCTGAGA 420
 QY 655 TCCATATTAGTCTCAGATCGCCGTTTTTTCTCTGACAGGCTTAAAGCTACTCTCCCA 714

Db 421 TCCATATTAGTCTCAGATCGCCGTTTTTCTCTGACAGGCTTAAAGCTACTCTCTTA 480
 QY 715 CTTGGCTTCCAGGCTTCGGCCCACTTACCTCCACCCGGTCTTCTGCGCGGATCG 774
 Db 481 CTTGGCTTCCAGGCTTCGGCCCACTTACCTCCACCCGGTCTTCTGCGCGGATCG 540
 QY 775 CTGGGCAAGGCTATGCTAGTGT 799
 Db 541 CTGGGCAAGGCTATGCTAGTGT 565
 RESULT 8
 ACH86315
 ID ACH86315 standard; DNA; 157 BP.
 AC ACH86315;
 DT 29-JUL-2004 (first entry)
 XX Human genome derived single exon probe #19510.
 DE Human genome derived single exon probe #19510.
 XX Human, probe; ss; gene expression; single exon probe; microarray;
 KM alternative splicing event; genomic alteration.
 OS Homo sapiens.
 PN US2003194704-A1.
 PD 16-OCT-2003.
 XX 03-APR-2002; 2002US-00029386.
 PF 03-APR-2002; 2002US-00029386.
 PR 03-APR-2002; 2002US-00029386.
 XX (PENN/) PENN S G.
 PA (FANK/) FANK D R.
 PA (HANK/) HANKEL D R.
 PI Penn SG, Rank DR, Hanzel DK;
 DR WPI; 2004-119264/12.
 XX New human genome-derived single exon nucleic acid probes useful for human
 PT gene expression analysis, for identifying or characterizing alternative
 PT splicing events, for assessing genomic alterations or as tools for
 PT surveying tissues.
 XX Claim 1; SEQ ID NO 19510; 80bp; English.
 PS The invention relates to a nucleic acid probe for measuring human gene
 CC expression, comprising any of the 27,400 fully defined nucleotide
 CC sequences in the specification, or their complements or fragments, and
 CC encoding at least 8 amino acids of any of the 688 amino acid sequences
 CC fully defined in the specification. The probe is a single exon probe that
 CC hybridises under high stringency conditions to a nucleic acid molecule
 CC expressed in human cells or tissues. Also included are a spatially-
 CC addressable set of single exon nucleic acid probes for measuring human
 CC gene expression (comprising a plurality of single exon nucleic acid
 CC probes cited above, where each of the plurality of probes is separately
 CC and addressably isolatable or amplifiable from the plurality), a single
 CC exon microarray for measuring human gene expression, a method of
 CC measuring human gene expression, a vector comprising the single exon
 CC probe cited above, an ORF-encoded peptide comprising at least 8
 CC contiguous amino acids of any of the above-mentioned amino acid
 CC sequences (optionally with conservative amino acid substitutions), an
 CC isolated antibody that binds specifically to a peptide cited above,
 CC methods of selling and/or licensing single exon probes or microarrays to
 CC a customer desiring to measure gene expression, a method of providing
 CC human gene expression data by subscription, and a computer-readable
 CC storage medium which contains a database having a plurality of records
 CC (each record including data on the expression of a single exon probe
 CC cited above. The probe, methods and apparatus are useful in gene
 CC expression analysis. The probes may be used as tools for surveying

CC tissues to detect the presence of expressed messages that contain their
CC specific exon, or in constructing genome-derived single exon microarrays.
CC In addition, the probes are used in identifying and characterizing
CC alternative splicing events, in detecting and characterizing gross
CC alterations in the genomic locus that includes their exon, in assessing
CC smaller genomic alterations, in priming the synthesis of nucleic acids,
CC or in expressing the ORF-encoded peptide. The present sequence is a human
CC single exon probe of the invention. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?docid=20030194704
CC
SQ Sequence 157 BP; 38 A; 64 C; 38 G; 17 T; 0 U; 0 Other;

Query Match 17.6%; Score 157; DB 12; Length 157;
Best Local Similarity 100.0%; Pred. No. 1.8e-31;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 318 ACCGCTAGAACGATCTCTCACTCCCGGCTGACGACCTTGGCCGAGAC 377
DB 1 ACCGCTAGAACGATCTCTCACTCCCGGCTGACGACCTTGGCCGAGAC 60
QY 378 CCAAGCCCCAGAAAACCTGAGCTCTGCTGCTGAGTGGACAAACGACTTCAAGAGA 437
DB 61 CCAAGCCCCAGAAAACCTGAGCTCTGCTGCTGAGTGGACAAACGACTTCAAGAGA 120
QY 438 GCCAGACTAGACCCACCCCGGAGAGTACAGTAA 474
DB 121 GCCAGACTAGACCCACCCCGGAGAGTACAGTAA 157

RESULT 9

ADC86738/C
ID ADC86738 standard; DNA; 3133 BP.

AC ADC86738;

DT 01-JAN-2004 (first entry)

DE Human GPCR gene SEQ ID NO:1191.

XX ds; gene; human; GPCR;

KM guanosine triphosphate-binding protein coupled receptor; gene therapy.

XX Homo sapiens.

OS Homo sapiens.

PN BP1270724-A2.

XX 02-JAN-2003.

PF 18-JUN-2002; 2002BP-00013517.

XX 18-JUN-2001; 2001JP-00246789.

PR (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.

PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATOR.

PI Suwa M, Asai K, Akiyama Y, Aburatani H;

XX WPI; 2003-315783/31.

DR P-PSDB; ADC86739.

XX New polynucleotide, useful for preparing a composition for treating a

PT patient in need of increased or suppressed activity or expression of the

PT guanosine triphosphate-binding protein coupled receptor.

XX Claim 1; SEQ ID NO 1191; 28pp; English.

XX The invention relates to a novel polynucleotide encoding a guanosine

CC triphosphate-binding protein coupled receptor (GPCR). A polynucleotide of

CC the invention may have a use in gene therapy. The polynucleotide and

CC polypeptide are useful for preparing a composition for treating a patient

CC in need of increased or suppressed activity or expression of the

CC guanosine triphosphate-binding protein coupled receptor. The
CC polynucleotide sequences shown in ADC85548-ADC87616 encode GPCR's of the
CC invention.

SQ Sequence 3133 BP; 95 A; 51 C; 821 G; 55 T; 0 U; 2111 Other;

Query Match 6.9%; Score 61.8; DB 10; Length 3133;
Best Local Similarity 33.4%; Pred. No. 6.9e-06;
Matches 207; Conservative 0; Mismatches 413; Indels 0; Gaps 0;

QY 132 CAGAGGCGACCTCTTCAACCCACCGAGAGACCGAGAGAGAGAGCTCCCAACATT 191
DB 983 CANNNNCC 924
QY 192 GCCTCAGAGGCCCCCACTCCCGGTGACCTTGAGGAGAGGAGACCCCTCTTTGAAGA 251
DB 923 CCNCCNCCNCCCN 864
QY 252 TCCCTCGCTAACCGCCGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 311
DB 863 NCCCCCCCCNCCGCCCNCCNCCGCCCNCCNCCGCCCNCCNCCGCCCNCCNCCGCC 804
QY 312 CCCTGAAACGCTGAAACGATCTCTCACTCTCCGAGCTGACGACCTTGGCCGAC 371
DB 803 CCCCCCCCCNCCGCCCNCCNCCGCCCNCCNCCGCCCNCCNCCGCCCNCCNCCGCC 744
QY 372 AGAACCCGACCCCGAGAAAACCTGAGCTCTGCTGCTGCTGAGTGAACAACGACCTCA 431
DB 743 NCCCCCCCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCN 684
QY 432 GAGAGAGCAGACCTAGACCCACCGAGAGAGTACAGATTAATGAGTCCCTCAGCCG 491
DB 683 CANNNNCC 624
QY 492 TCTGTTCCAGAGGATCTCAAGAGACGACCTCTGCACTCTGATTTCCCGTGAAT 551
DB 623 CANNCCNCCNCC 564
QY 552 TCTTCCCAATTTAGCTATCTCTTAACCTCTTCTGATTTCCCGTGAAT 611
DB 563 CCCCCCCCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCN 504
QY 612 CCGGTAGGTGATGTTCTCAATATTTCTGCTGCTGCTGCTGCTGCTGCTGCTG 671
DB 503 CACCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCN 444
QY 672 CATCGCCGCTTTTCTCTGACAGCCTTACTCTTCTGCTGCTGCTGCTGCTGCTG 731
DB 443 CCCCCCCCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCN 384
QY 732 GGCCTCACTTCTCCACG 751
DB 383 NNNNNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCN 364

RESULT 10

ABN32329
ID ABN32329 standard; DNA; 60 BP.

AC ABN32329;

DT 15-JUL-2002 (first entry)

DE Human spliced transcript detection oligonucleotide SEQ ID NO:5077.

XX Human; mouse; rat; splice transcript; detection; RNA transcript;

KM splice variant; transcriptome; oligonucleotide library; ss.

XX Homo sapiens.

OS Homo sapiens.

PN WO200210449-A2.

XX 07-FEB-2002.

XX 20-JUL-2001, 2001WO-IB001903.
PF
XX
PR 28-JUL-2000, 2000US-0231607P.
PR 02-MAY-2001, 2001US-0287724P.
XX
XX
XX (COMP-) COMPUGEN INC.
XX Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S,
XX WPI, 2002-25383/30.
DR
XX
XX
PT New oligonucleotide libraries comprising oligonucleotides which
PT selectively hybridize to mRNAs transcribed from a transcription unit of a
PT genome, useful for detecting tissue-, pathology-, and developmental-
PT specific genes.
XX
XX Example 1; SEQ ID NO 5077, 47bp, English.
XX
XX The present invention describes oligonucleotide libraries for detecting
XX messenger RNAs that populate a (sub-)transcriptome, where the (sub-
XX) transcriptome comprises messenger RNAs transcribed from multiple
XX transcription units that populate a genome. The library comprises several
XX oligonucleotides, each capable of hybridizing selectively to a set of
XX messenger RNAs transcribed from a given transcription unit of the genome,
XX which encodes one or more messenger RNA splice variants. The
XX oligonucleotide libraries are useful for detecting mRNAs from a
XX biological sample, in expression profiling studies, in qualitatively or
XX quantitatively characterizing the corresponding transcriptome, and in
XX detecting RNA transcripts and splice variants of human or animal
XX transcriptomes. The libraries may also be used as specialized mini
XX libraries to detect transcripts of a sub-transcriptome under a particular
XX biological or pathological state, and so allowing the detection of tissue
XX - and pathology-specific genes such as those genes only expressed in
XX specific tissue under a specific pathological condition; to detect
XX developmental specific genes; and to detect RNA transcripts and splice
XX variants of a transcriptome of a patient suffering from a particular
XX disorder. AHN27253 to AHN59589 represent oligonucleotide sequences from
XX rats, humans and mice, which are used in the exemplification of the
XX present invention. N.B. The sequence data for this patent did not form
XX part of the printed specification, but was obtained in electronic format
XX directly from WIPO at ftp.wipo.int/pub/published_pat_sequences
XX
XX Sequence 60 BP, 11 A; 25 C; 5 G; 19 T; 0 U; 0 Other;
SQ
Query Match 6.7%; Score 60; DB 6; Length 60;
Best Local Similarity 100.0%; Pred. No. 5.4e-06;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 522 GCCCTCTCCACCCCTGATTCCTCCGTAATCTTCCCAATTTAGCCCTATCTCTTAACC 581
DB 1 GCCCTCTCCACCCCTGATTCCTCCGTAATCTTCCCAATTTAGCCCTATCTCTTAACC 60
RESULT 11
AAZ17263
ID AAZ17263 standard; cDNA, 1337 BP.
XX
XX AAZ17263;
XX
XX 12-OCT-1999 (first entry)
XX
XX Human gene expression product cDNA sequence SEQ ID NO:4735.
XX
XX Human; gene; gene expression product; diagnosis; therapy; probe;
XX detection; mapping; tissue typing; profiling; forensic; cancer;
XX genetic analysis; colorectal cancer; breast cancer; lung cancer; ss.
XX Homo sapiens.
XX
XX MO9938972-A2.
XX PN
XX 05-AUG-1999.
PD

XX 28-JAN-1999, 99MO-US001619.
XX
XX
XX 28-JAN-1998, 98US-0072910P.
PR 24-FEB-1998, 98US-0075954P.
PR 31-MAR-1998, 98US-0080114P.
PR 03-APR-1998, 98US-0080515P.
PR 03-APR-1998, 98US-0080666P.
PR 21-OCT-1998, 98US-0105234P.
PR 28-OCT-1998, 98US-0105877P.
XX
XX (CHIR) CHIRON CORP.
XX (HYSE-) HYSEQ INC.
XX
XX Williams LT, Escobedo J, Innis MA, Garcia PD, Sudduth-Klinger J;
XX Reinhard C, Giese K, Randazzo F, Kennedy GC, Pot D, Kassem A,
XX Lemson G, Drmanac R, Ckvenjakov R, Dickson M, Drmanac S, Labat I,
XX Leshkowitz D, Kita D, Garcia V, Jones WL, Stache-Crain B,
XX WPI, 1999-494092/41.
XX
XX
XX Novel human genes and their expression products which are differentially
XX expressed in different cell types.
XX
XX Claim 1; Page 2250-2251, 2479pp; English.
XX
XX The present invention describes a library of human polynucleotides
XX comprising the sequences given in AAZ12532 to AAZ17779. Also described is
XX a method of detecting differentially expressed genes correlated with the
XX cancerous state of a mammalian cell, comprising detecting at least one
XX differentially expressed gene product in a test sample from a cell
XX suspected of being cancerous, where the gene product is encoded by one of
XX the 5248 polynucleotide sequences given in AAZ12532 to AAZ17779. The
XX polynucleotides can be used as a source of primers and probes, which can
XX be used for a variety of purposes, e.g. detection of expression levels,
XX mapping, tissue typing or profiling, forensics, genetic analysis and
XX detection of polymorphisms. Polypeptides encoded by the polynucleotides
XX can be used for raising antibodies for experimental, diagnostic and
XX therapeutic purposes. The polynucleotides may also be used to construct
XX arrays for diagnostics (which may be used to determine function of an
XX encoded protein); and to detect differences in expression levels between
XX two cells (e.g. to identify abnormal or diseased tissue in a human, to
XX identify a genetic predisposition or susceptibility to a disease such as
XX cancer). The polynucleotides of the invention are especially used in the
XX diagnosis, prognosis and management of colorectal cancer, breast cancer,
XX and lung cancer. The polynucleotides can also be used to screen for
XX peptide analogues and antagonists
XX
XX Sequence 1337 BP, 42 A; 577 C; 27 G; 22 T; 0 U; 669 Other;
SQ
Query Match 6.2%; Score 55; DB 2; Length 1337;
Best Local Similarity 25.9%; Pred. No. 0.00032;
Matches 192; Conservative 0; Mismatches 549; Indels 1; Gaps 1;
QY 33 CCACCCCAGCTTTGGGGGCGAGTACATGATGATCTCAACTGAGAGCTCTGGGGAT 92
DB 346 CNNCCCCGNN 405
QY 93 CCGTGTCTTTTGGCTGCAACCAAGGAGATCTCAGGACGAGGCAACCTCTTACCC 152
DB 406 NNNCCCCGNN 465
QY 153 ACCCGAGAGGACCGAGAGAGGACAGGCTCCCAACTTGGCTCAGAGGCCCCAGTCC 212
DB 466 CCCCNN 525
QY 213 CGGTGACCTTTGGCCAGGGGACACCCCTCTTTTGAAGATCTCGGCTTACCCGCCAG 272
DB 526 NCCGNNCCGNNCCGNNCCGNNCCGNNCCGNNCCGNNCCGNNCCGNNCCGNNCCGNN 585
QY 273 TGTGCTGTGAGAGACTGCTGTAAGCTGAGTCTGAGCCCTGGAACGCGCTTGAAGAGGA 332
DB 586 CCCNNCCGNNCCGNNCCGNNCCGNNCCGNNCCGNNCCGNNCCGNNCCGNNCCGNNCCGNN 645

CC host cells comprising the fusion promoters, a method of identifying genes
 CC involved in cellular proliferation or required for proliferation of a
 CC prokaryotic cell using the vector, a method of identifying compounds that
 CC inhibit the proliferation of a prokaryotic cell using the vector, a
 CC method of identifying a compound that reduces the activity or level of a
 CC gene product required for proliferation of a cell using the vector, a
 CC compound identified by the methods, a method of inhibiting the activity
 CC or expression of a gene in an operon required for proliferation using the
 CC vector, manufacturing an antibiotic comprising using the vector or cell
 CC and identifying a nucleic acid with promoter activity in *Enterococcus*
 CC faecalis. The fusion promoters are useful for regulating nucleic acid or
 CC polypeptide expression, particularly for regulating gene expression in
 CC bacteria and for identifying proliferation-regulated genes or molecules
 CC with potential antibiotic activity. The modified promoters are also
 CC useful for replacing endogenous promoters to create cells with specific
 CC regulatable genes. The present sequence is vector (or fragment)
 CC incorporating a fusion promoter sequence of the invention
 CC
 XX
 SQ Sequence 12733 BP; 3549 A; 2567 C; 3207 G; 3409 T; 0 U; 1 Other;

Query Match 5.8%; Score 51.8; DB 6; Length 12733;
 Best Local Similarity 42.2%; Pred. No. 0.0048;

Matches 293; Conservative 0; Mismatches 402; Indels 0; Gaps 0;

QY 75 CTGGAGCTCTCGGGAGTCTGCTCTTGGCTGCACACAGGACATCTCAGGACGCA 134
 DB 5473 CTGGCGGACACTGTCTTACAGATTGATGAAGAAGACATGAAGTGGCGGACGA 5414
 QY 135 GGGGCACTCTTCACCCACCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 194
 DB 5413 TAGTCATGCCCCCGCCGACCGAAGAGAGTGAAGTGAAGGCTTCAAGGGCATCG 5354
 QY 195 TCAGGGGCCCCCAATCCCGGTGACCTTGGCCAGAGGAGAGAGAGAGAGAGAGAG 254
 DB 5353 GTGCACC 5294
 QY 255 TCCGCTACCCGCGCCGAGTGTCCCTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 314
 DB 5293 CC 524
 QY 315 TGAACGCGCTAGAAAGGATCTCTCAACCTCCCGGCGTGAAGAGAGAGAGAGAG 374
 DB 5233 CC 5174
 QY 375 ACCCGACCCCGCAGAAAAACCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 434
 DB 5173 CC 5114
 QY 435 GAGGCGAGAGCTAGAGACGACCCGAGAGAGATGAGATGAGATGAGATGAGATGAG 494
 DB 5113 CC 5054
 QY 495 TGTTCGAGGATCTGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 554
 DB 5053 CC 4994
 QY 555 TCCCAATTAGGCTATCTCTTAAGCTCTTCTCATCTCCGCTTTATTTGAAACC 614
 DB 4993 CC 4934
 QY 615 GTAAGTGTGTGTCTCAATATTTCTGTGCTCTGAGATGCATGATGATGCTGACAT 674
 DB 4933 CC 4874
 QY 675 CGCCCGTTTTTCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 734
 DB 4873 CC 4814
 QY 735 CCACCTACTCTCCACCCGCTTCTGCGCGCG 769
 DB 4813 CC 4779

RESULT 15

ACD13882/c
 ID ACD13882 standard; DNA; 12733 BP.

AC ACD13882;

DT 15-AUG-2003 (first entry)

DE L. lactis promoter containing plasmid pBPER14.

XX Promoter; de; gram positive bacteria; *Staphylococcus aureus*; plasmid;

KM *Enterococcus faecalis*; operator; xy10; tco; trp; mal0; lambda-cl0;

KW cellular proliferation.

OS *Lactococcus lactis*.

OS Synthetic.

PN US2003027286-A1.

PD 06-FEB-2003.

PP 21-DEC-2001; 2001US-00032393.

PR 06-SEP-2000; 2000US-0230335P.

PR 27-DEC-2000; 2000US-0259434P.

PA (HASELBECK R.

PA (WALL D.

PA (GROSS M.

PI HASELBECK R, Wall D, Gross M;

XX WPI: 2003-479541/45.

XX Example 3; Page 86-92; 142pp; English.

XX The invention relates to an isolated nucleic acid comprising a fusion

CC promoter having at least one promoter that is modified to have altered

CC activity in at least one gram-positive organism (e.g. *Staphylococcus*

CC *aureus* or *Enterococcus faecalis*). The promoter is linked to at least one

CC operator selected from xy10, tco, trp, mal0 and lambda-cl0, which are

CC positioned such that the binding of at least one repressor to the

CC operator represses transcription from the fusion promoter. Also included

CC are a vector comprising the isolated nucleic acid, a host cell comprising

CC the nucleic acid. The fusion promoter is useful for identifying genes

CC involved in cellular proliferation, identifying a compound that reduces

CC the activity or level of a gene product required for proliferation of a

CC cell, inhibiting the activity or expression of a gene in an operon

CC required for proliferation, manufacturing an antibiotic, identifying a

CC gene that is required for proliferation of a prokaryotic cell,

CC identifying a compound that inhibits the proliferation of a prokaryotic

CC cell and regulating gene expression in bacteria. The present sequence is

CC a plasmid containing a fusion promoter of the invention

XX
 SQ Sequence 12733 BP; 3549 A; 2567 C; 3207 G; 3409 T; 0 U; 1 Other;

Query Match 5.8%; Score 51.8; DB 9; Length 12733;

Best Local Similarity 42.2%; Pred. No. 0.0048;

Matches 293; Conservative 0; Mismatches 402; Indels 0; Gaps 0;

QY 75 CTGGAGCTCTCGGGAGTCTGCTCTTGGCTGCACACAGGACATCTCAGGACGCA 134
 DB 5473 CTGGCGGACACTGTCTTACAGATTGATGAAGAAGACATGAAGTGGCGGACGA 5414
 QY 135 GGGGCACTCTTCACCCACCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 194
 DB 5413 TAGTCATGCCCCCGCCGACCGAAGAGAGTGAAGTGAAGGCTTCAAGGGCATCG 5354

QY	121	ATCTCAGG	CAGGAGG	CCACCCCTCTCA	CCACCCGAGAGGA	CCGAGAGG	CGGAGG	180
QY	121	ATCTCAGG <th>CAGGAGG</th> <th>CCACCCCTCTCA</th> <th>CCACCCGAGAGGA</th> <th>CCGAGAGG</th> <th>CGGAGG</th> <td>180</td>	CAGGAGG	CCACCCCTCTCA	CCACCCGAGAGGA	CCGAGAGG	CGGAGG	180
Db	121	ATCTCAGG <th>CAGGAGG</th> <th>CCACCCCTCTCA</th> <th>CCACCCGAGAGGA</th> <th>CCGAGAGG</th> <th>CGGAGG</th> <td>180</td>	CAGGAGG	CCACCCCTCTCA	CCACCCGAGAGGA	CCGAGAGG	CGGAGG	180
QY	181	TCGCCAACA <td>TTTGCTCAGG</td> <td>GGCCCCCAGTCC</td> <td>CCGGTGA</td> <td>CCCTTG</td> <td>GGCCAGGG</td> <td>CA</td>	TTTGCTCAGG	GGCCCCCAGTCC	CCGGTGA	CCCTTG	GGCCAGGG	CA
Db	181	TCGCCAACA	TTTGCTCAGG	GGCCCCCAGTCC	CCGGTGA	CCCTTG	GGCCAGGG	CA
QY	241	CTCTTTGA	AGATCCCTCG	CTACCCGCTAC	GGTTCCTTGA	GAACTG	CTGTA	ACT
Db	241	CTCTTTGA	AGATCCCTCG	CTACCCGCTAC	GGTTCCTTGA	GAACTG	CTGTA	ACT
QY	301	GGAGTCTG	AGCCCTTGAA	CCGCTTAAG	AGGATCTCTCA	ACTCCCG	GGCTG	AGC
Db	301	GGAGTCTG	AGCCCTTGAA	CCGCTTAAG	AGGATCTCTCA	ACTCCCG	GGCTG	AGC
QY	361	CCTTGGCC	GGCAGAG	CCCCAG	CCCCAG	AAAA	CCCTGG	CCCTG
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QY	421	AACCGA	CCCTCAG	AGAGG	CCAGAC	CTTAC	CCCGG	AGAG
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QY	481	CCCTCAG	CCGTTCTG	TTCCAG	GCATCTC	CAAG	CCAC	CCCTG
Db	481	CCCTCAG	CCGTTCTG	TTCCAG	GCATCTC	CAAG	CCAC	CCCTG
QY	541	TCGCCGTGA	ATTCTTCC	CAATTAG	CTATCTCTT	AAAC	CTTCTC	ATTCC
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QY	601	TTTATTCTGA	ACCCGTAAG	GGGTGTTC	CAATATTTCC	GTCCCTCC	CTGAT	CCATA
Db	601	TTTATTCTGA	ACCCGTAAG	GGGTGTTC	CAATATTTCC	GTCCCTCC	CTGAT	CCATA
QY	661	CTTAGTCTC	ACATG	GC	CCGTTTTC	CTCTGA	GC	CTTAA
Db	661	CTTAGTCTC	ACATG	GC	CCGTTTTC	CTCTGA	GC	CTTAA
QY	721	CTCCAGG	GCTCGG	CCCCCA	CTACCTCC	ACCGG	TTCTCG	CCCGG
Db	721	CTCCAGG	GCTCGG	CCCCCA	CTACCTCC	ACCGG	TTCTCG	CCCGG
QY	781	CAGG	CTATG	TA	CTG	CTG	CTG	CTG
Db	781	CAGG	CTATG	TA	CTG	CTG	CTG	CTG
QY	841	AGACAG	CTGCTG	CTTCA	TGA	ACG	AAAAA	TA
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Query Match	99.8%	Score 889.4	DB 6	Length 1143
Best Local Similarity	99.9%	Pred. No. 5.9e-192		
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1	CCCTTTGGGGTTCCAGGCA	CCCAACTCAGCCCA	CCCCAGCTTTGGGGGCGAGTACATA	60
253	CCTCTGGGGTCCAGGCA	CCCAACTCAGCCCA	CCCCAGCTTTGGGGGCGAGTACATA	312
61	GCCATGATCTCACTGGA	AGGCTCTGGGAGTCTGGT	CTTTGGCTCACAACAGAGGC	120
313	GCCATGATCTCACTGGA	AGGCTCTGGGAGTCTGGT	CTTTGGCTCACAACAGAGGC	372
121	ATCTCAGGACGAGAGG	CAACCCCTCTCAACC	CAACCCGAGAGACCGAGAGGCAAGC	180
373	ATCTCAGGACGAGAGG	CAACCCCTCTCAACC	CAACCCGAGAGACCGAGAGGCAAGC	432
161	TCCCAACATTTGCTCA	GAGGCGCCCACTGCCCCGGTGA	CCCTTGGCCAGGGGCAACCCCT	240
433	TCCCAACATTTGCTCA	GAGGCGCCCACTGCCCCGGTGA	CCCTTGGCCAGGGGCAACCCCT	492
241	CTCTTTGAAATTCCTG	CGGCTTACC	CGCCCAAGTGGTCTTGAGAGACTGCTCGTAAACT	300
493	CTCTTTGAAATTCCTG	CGGCTTACC	CGCCCAAGTGGTCTTGAGAGACTGCTCGTAAACT	552
301	GGAAGTCTGGCCCCCT	GAAACCGGCTTAAAGAGGAT	CTCTCTCAACTCCCGGCTCGACGAC	360
553	GGAAGTCTGGCCCCCT	GAAACCGGCTTAAAGAGGAT	CTCTCTCAACTCCCGGCTCGACGAC	612
361	CCTTGGCGGAGAGAC	CCCAAGCCCTCAAGAAAC	CCCTGACCTCTGACGCTGAGTGAAC	420
613	CCTTGGCGGAGAGAC	CCCAAGCCCTCAAGAAAC	CCCTGACCTCTGACGCTGAGTGAAC	672
421	AACGACCTCAAGAGAG	ACAGACTTGAACCC	CCCGGAGAGTACAGATTAATGAAT	480
673	AACGACCTCAAGAGAG	ACAGACTTGAACCC	CCCGGAGAGTACAGATTAATGAAT	732
481	CCCGCTCAGGCGCTG	CTGTTCCAGGCACTCTCAGG	CAACCAAGCCCTGCAACCTCGAT	540
733	CCCGCTCAGGCGCTG	CTGTTCCAGGCACTCTCAGG	CAACCAAGCCCTGCAACCTCGAT	792
541	TCGCCGTGAATCTTCC	CAATTAGCCTATCTCTTAAAC	CTCTCTCTCAATTCCTCGGT	600
793	TCGCCGTGAATCTTCC	CAATTAGCCTATCTCTTAAAC	CTCTCTCTCAATTCCTCGGT	852
601	TTTATTCGAAACCGGT	TAAGTGGTCTCAATTTTCTG	TCTGCCCTCGAGATCCATA	660
853	TTTATTCGAAACCGGT	TAAGTGGTCTCAATTTTCTG	TCTGCCCTCGAGATCCATA	912
661	CTTAGTCTCAATGAG	CCGCTTTTCTGAGAGGCTAAG	CTACTCTCTCACTCGC	720
913	CTTAGTCTCAATGAG	CCGCTTTTCTGAGAGGCTAAG	CTACTCTCTCACTCGC	972
721	CTCAGAGCTCTGGG	CCCACTACTCCCAACCGGCT	CTTCTGCGCGGAGTGGTGGG	780
973	CTCAGAGCTCTGGG	CCCACTACTCCCAACCGGCT	CTTCTGCGCGGAGTGGTGGG	840
781	CAGGAGTATGATCTG	TTCCCTTCCGACACCTGGTGG	CGGCGGAGGAACTATCAGT	891
1033	CAGGAGTATGATCTG	TTCCCTTCCGACACCTGGTGG	CGGCGGAGGAACTATCAGT	1092
841	AGACAGCTGCTGCTT	CCATGAAACGAAAAATAAAT	ATCATGTTTTCTTAA	891
1093	AGACAGCTGCTGCTT	CCATGAAACGAAAAATAAAT	ATCATGTTTTCTTAA	1143

LOCUS AF484420 1185 bp mRNA linear PRI 02-MAR-2003
DEFINITION Homo sapiens psoriasis susceptibility 1 candidate 2 (PSORS1C2)
ACCESSION AF484420
VERSION AF484420.1 GI:28628934
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1185)
Hollm, S.J., O'Brien, K.P., Carlen, L. and Stahle-Backdahl, M.
The PSORS1C1 and PSORS1C2 genes in 6p21.3 associate strongly with
psoriasis in the Swedish population
JOURNAL Unpublished
2 (bases 1 to 1185)
Hollm, S.J., O'Brien, K.P., Carlen, L. and Stahle-Backdahl, M.
Direct Submission
Submitted (15-FEB-2002) Dermatology, Karolinska Institute, L8:02
Karolinska Sjukhuset, Stockholm S-17176, Sweden
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Query Match 99.8%; Score 889.4; DB 9; Length 1185;
Best Local Similarity 99.8%; Pred. No. 5.9e-192;
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QY 1 CCTTTGGGGTTCACAGGACCCAGACTCAGCCACCCAGCTTTGGGGGCGCAGTACATA 60
DB 262 CTTCTGGGGTTCACAGGACCCAGACTCAGCCACCCAGCTTTGGGGGCGCAGTACATA 321
QY 61 GCCATGATCCCTCACTGGAAGCTCTGGGGAATCTGGTCTTTGCTGCACACAGAGGC 120
DB 322 GCCATGATCCCTCACTGGAAGCTCTGGGGAATCTGGTCTTTGCTGCACACAGAGGC 381
QY 121 ATCTCAGCAGCAGGAGCCCTCTCACCACCCAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
DB 382 ATCTCAGCAGCAGGAGCCCTCTCACCACCCAGAGAGAGAGAGAGAGAGAGAGAGAGAG 441
QY 181 TCCCAACATTGCTCTCAGGGGCCCCCAGTCCCGGTGACCTTTGGCCAGGGGCAACCCCT 240
DB 442 TCCCAACATTGCTCTCAGGGGCCCCCAGTCCCGGTGACCTTTGGCCAGGGGCAACCCCT 501
QY 241 CTTCTTAAAGTCTCCGCGCTCAGCGGCGCAGTGTCTCCGAGAGAGAGAGAGAGAGAG 300
DB 502 CTTCTTAAAGTCTCCGCGCTCAGCGGCGCAGTGTCTCCGAGAGAGAGAGAGAGAGAG 561
QY 301 GAGTCTGAGCCCTGAGACCGCTAGAACGATCTCTCAACTCCCGCGCTGAGAGAC 360
DB 562 GAGTCTGAGCCCTGAGACCGCTAGAACGATCTCTCAACTCCCGCGCTGAGAGAC 621
QY 361 CTTTGGCGGAG 420
DB 622 CTTTGGCGGAG 681

QY 421 AACGACCTCAG 480
DB 682 AACGACCTCAG 741
QY 481 CCCCTCAGCCGTTCTGTTCCAGGACATCTCAGGACACCCAGCCCTCTCACTCTGAT 540
DB 742 CCCCTCAGCCGTTCTGTTCCAGGACATCTCAGGACACCCAGCCCTCTCACTCTGAT 801
QY 541 TCCCGGGAATCTCCCAATTTAGGCTATCTCTTAAACCTCTTCCTCACTCCCTGGT 600
DB 802 TCCCGGGAATCTCCCAATTTAGGCTATCTCTTAAACCTCTTCCTCACTCCCTGGT 861
QY 601 TTATTTGAAACCGGTAGAGGTGTCTCAATATTTCTGTCCCTCTCAGATCCATA 660
DB 862 TTATTTGAAACCGGTAGAGGTGTCTCAATATTTCTGTCCCTCTCAGATCCATA 921
QY 661 CTTATGCTCAGATCGCCCGCTTTTCTCTGACAGCTTAAGCTACTCTCTCACTCGC 720
DB 922 CTTATGCTCAGATCGCCCGCTTTTCTCTGACAGCTTAAGCTACTCTCTCACTCGC 981
QY 721 CTCAGGCTCGGCGCCACCTACCTCCACCGGTTCTCTGCGCGGAGTGGTGGG 780
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QY 781 CAGGCTATGATCTGTGTTCCCTTGCACCTGTGTGGCGGCGAGAGATATCAGT 840
DB 1042 CAGGCTATGATCTGTGTTCCCTTGCACCTGTGTGGCGGCGAGAGATATCAGT 1101
QY 841 AGACAGCTGCTGCTTCATGAAACGAAATATTAATCATGTTTCTTAA 891
DB 1102 AGACAGCTGCTGCTTCATGAAACGAAATATTAATCATGTTTCTTAA 1152
RESULT 4
AX406002
LOCUS AX406002 1473 bp DNA linear PAT 14-JUN-2002
DEFINITION Sequence 417 from Patent WO0222660.
ACCESSION AX406002
VERSION AX406002.1 GI:21439443
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
Yang, Y.T., Liu, C., Zhou, P., Asundi, V., Zhang, J., Zhao, Q.A., Ren, F.,
Xue, A.J., Yang, Y., Wehrman, T. and Drmanac, R.T.
Novel nucleic acids and polypeptides
Patent: WO 0222660-A 417 21-MAR-2002;
HYSBO, INC. (US)
FEATURES
source location/Qualifiers
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Query Match 99.5%; Score 886.2; DB 6; Length 1473;
Best Local Similarity 99.7%; Pred. No. 3.1e-191;
Matches 889; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 CCTTTGGGGTTCACAGGACCCAGACTCAGCCACCCAGCTTTGGGGGCGCAGTACATA 60
DB 573 CTTCTGGGGTTCACAGGACCCAGACTCAGCCACCCAGCTTTGGGGGCGCAGTACATA 632

Db 733 CCCCTGACCGCTCTGTTCCAGGCAATCTCCAGGACCAACGCCCTCTCCACCTCTGAT 792
Qy 541 TCCCGTGAATCTTCCCAATTTAGCCATCTCTCTTAACCTTCTCCATTCCTCGGT 600
Db 793 TCCCGTGAATCTTCCCAATTTAGCCATCTCTCTTAACCTTCTCTCATTTCCCTGGT 852
Qy 601 TTATATCTGAACCCGTAAGGTGTGTTCTCAATAATTTCTGTCCCTCTGTAGATTCATA 660
Db 853 TTATATCTGAACCCGTAAGGTGTGTTCTCAATAATTTCTGTCCCTCTGTAGATTCATA 912
Qy 661 CTTAGTCTCAATCGCCCTTTTCTCTGTACAGCTTAAGCTTACTCTCACTCTG 720
Db 913 CTTAGTCTCAATCGCCCTTTTCTCTGTACAGCTTAAGCTTACTCTCACTCTG 972
Qy 721 CTCAGGCTCTGCGCCCACTCACTCCACCCGGTCTTCCGCGCGGCGATGCTG 780
Db 973 CTCAGGCTCTGCGCCCACTCACTCCACCCGGTCTTCCGCGCGGCGATGCTG 1032
Qy 781 CAGGCTATGGAATCTGTTTCCCTTCTGCACTGTGTGCGCGGCGAGAACTATGAT 840
Db 1033 CAGGCTATGGAATCTGTTTCCCTTCTGCACTGTGTGCGCGGCGAGAACTATGAT 1092
Qy 841 AGACAGCTGCTGCTTCCATGAAACGAAATAAATCATGTTTCTTAA 891
Db 1093 AGACAGCTGCTGCTTCCATGAAACGAAATAAATCATGTTTCTTAA 1143
RESULT 6
AX477396 2997 bp DNA linear PAT 12-AUG-2002
LOCUS Sequence 10 from Patent WO244375.
DEFINITION AX477396
ACCESSION AX477396
VERSION AX477396.1 GI:22216625
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS Charnley, P., Moss, P. and Mceuen, M.
TITLE Compositions and methods for diagnosing or treating psoriasis
JOURNAL Patent: WO 0244375-A 10 06-JUN-2002;
Celltech R & D, Inc. (US)
FEATURES
source Location/Qualifiers
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Query Match 87.0%; Score 775.4; DB 6; Length 2997;
Best Local Similarity 99.9%; Pred. No. 4.9e-166;
Matches 776; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 115 AGAGGATCTCAGGCGAGGAGGCGACCCCTCTACACCCGCGAGAGACCGAGAGAG 174
Db 2198 ACAGGATCTCAGGCGAGGAGGCGACCCCTCTACACCCGCGAGAGACCGAGAGAG 2257
Qy 175 GCAAGCTCCCAACATTGCTCAGAGGCGCCCACTGCCGTGACCTTGGCGAGGAGCA 234
Db 2258 GCAAGCTCCCAACATTGCTCAGAGGCGCCCACTGCCGTGACCTTGGCGAGGAGCA 2317
Qy 235 CCCCCTCTTTGAAGATCTCGGCTTACCGGCCGAGTGTCTCTGAGAGACTGCT 294
Db 2318 CCCCCTCTTTGAAGATCTCGGCTTACCGGCCGAGTGTCTCTGAGAGACTGCT 2377
Qy 295 GAAAGTGAAGTGTGCGCCGCGAGCGGCTTGAAGAGATCTCTCAACCTCCCGGCT 354
Db 2378 GAAAGTGAAGTGTGCGCCGCGAGCGGCTTGAAGAGATCTCTCAACCTCCCGGCT 2437
Qy 355 GAGGACCTTGTGCGGAGGAGACCCGAGCCCGCGAGAAACCTTGTGCTGCGCTGAG 414
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Qy 415 GTGACAAACGACTCAGAGAGAGCCAGACTAGACCCACCCGGAGAGATACAGATA 474
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RESULT 7
AX477390 3001 bp DNA linear PAT 12-AUG-2002
LOCUS Sequence 4 from Patent WO244375.
DEFINITION AX477390
ACCESSION AX477390
VERSION AX477390.1 GI:22216619
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS Charnley, P., Moss, P. and Mceuen, M.
TITLE Compositions and methods for diagnosing or treating psoriasis
JOURNAL Patent: WO 0244375-A 4 06-JUN-2002;
Celltech R & D, Inc. (US)
FEATURES
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Query Match 87.0%; Score 775.4; DB 6; Length 3001;
Best Local Similarity 99.9%; Pred. No. 4.9e-166;
Matches 776; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 115 AGAGGATCTCAGGCGAGGAGGCGACCCCTCTACACCCGCGAGAGACCGAGAGAG 174
Db 2202 ACAGGATCTCAGGCGAGGAGGCGACCCCTCTACACCCGCGAGAGACCGAGAGAG 2261
Qy 175 GCAAGCTCCCAACATTGCTCAGAGGCGCCCACTGCCGTGACCTTGGCGAGGAGCA 234
Db 2262 GCAAGCTCCCAACATTGCTCAGAGGCGCCCACTGCCGTGACCTTGGCGAGGAGCA 2321
Qy 235 CCCCCTCTTTGAAGATCTCGGCTTACCGGCCGAGTGTCTCTGAGAGACTGCT 294
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QY 295 GAAATGAGATCTGGCCCTCCGTAACCCGCTAGAAAGCATCTCTCACTCCCGGCT 354
 Db 2382 GAAATGAGATCTGGCCCTCCGTAACCCGCTAGAAAGCATCTCTCACTCCCGGCT 2441
 QY 355 GACGACCTTGGCCCGGAGAGACCCAGCCCGGAGAAACCCCTGGCTCTGCCCCGAG 414
 Db 2442 GACGACCTTGGCCCGGAGAGACCCAGCCCGGAGAAACCCCTGGCTCTGCCCCGAG 2501
 QY 415 GTGAGACAACGCACTCGAGAGAGACCACTAGACCAACCCCGGAGAGATAGATTA 474
 Db 2502 GTGAGACAACGCACTCGAGAGAGACCACTAGACCAACCCCGGAGAGATAGATTA 2561
 QY 475 TGGAGTCCCTCAGCCGCTCTGTTCCAGGCACTCCAGGACCCAGCCCTCTCCACC 534
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RESULT 8
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 LOCUS Homo sapiens clone UMGc:y24c027 from 6p21, complete sequence.
 DEFINITION AC004195
 ACCESSION AC004195
 VERSION AC004195.1 GI:3980474
 KEYWORDS HTG.
 ORGANISM Homo sapiens (human)
 SOURCE Homo sapiens
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 40878)
 AUTHORS Janer,M., Guillaudoux,T., Vu,Q., Kutayavin,T., Harter,H. and Geraghty,D.E.
 TITLE Large scale sequence analysis of the human MHC class I region
 JOURNAL Unpublished (1998)
 REMARK The Hutchinson Cancer Research Center
 The Clinical Research Division
 1100 Fairview Ave. N., P.O. Box 19024
 Seattle, WA 98109-1024
 Contact: Daniel E. Geraghty (geraghty@fhcrc.org)
 2 (bases 1 to 40878)
 Geraghty,D.E. and Olson,M.V.
 REFERENCE Direct Submission
 AUTHORS Submitted (23-FEB-1998) Human Genome Center, University of Washington, Box 352145, Seattle, WA 98195, USA
 JOURNAL 3 (bases 1 to 40878)
 Geraghty,D.E. and Olson,M.V.
 REFERENCE Direct Submission
 AUTHORS Submitted (08-DEC-1998) Human Genome Center, University of Washington, Box 352145, Seattle, WA 98195, USA
 JOURNAL University of Washington Human Genome Center
 REMARK

COMMENT
 Box 352145 Seattle, WA 98195
 Contact: Daniel E. Geraghty (geraghty@fhcrc.org)
 On Dec 8, 1998 this sequence version replaced gi:2905865.
 Overlapping Sequences:
 5': UMGc:y14c057 (Genbank Accession: AC006047)
 3': UMGc:y14c203

Sequence Quality Assessment:
 This entry has been annotated with sequence quality estimates computed by the Phrap assembly program. All manually edited bases have been reduced to quality zero. Quality levels above 40 are expected to have less than 1 error in 10,000 bp.
 Base-by-base quality values are not generally visible from the Genbank flat file format but are available as part of this entry's ASN.1 file.

Double stranded (DS) coverage: 77.6%
 DS or two chemistry coverage: 100.0%
 Single stranded regions: 0

Sequence Validation:
 This sequence has been validated by Multiple Complete Digest Mapping. Comparison of the experimentally derived map digest fragments with sequence-predicted fragments is given below. Small fragments below a variable cutoff (approximately 400-600bp) are not mapped and hence do not appear in the table. There are no significant remaining discrepancies between the experimental and predicted values. Uniquely ordered fragment groups are separated by dashed lines.

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894.03	880.00	4618.79	4525.00	10116.87	9663.00
3041.57	2999.00	1532.79	1530.00	2432.75	2413.00
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ORIGIN

Matches 776; Conservative 0; Mismatches 1; Indels 0; Gaps 0

[illegible]

Matches 775; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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BD095297	The method of testing for perioritis vulgaris.	BD095297.1	GI:22640885	WO 0142458-A/2.	Homo sapiens (human)	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.	Inoko, H. and Tamiiya, G.	The method of testing for psoriasis vulgaris	HIDETOSHI INOKO, GEN TAMIIYA	OS Homo sapiens (human) PN WO 0142458-A/2 PD 14-JUN-2001
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REFERENCE
AUTHORS 1
TITLE Shima, T., Ota, M., Katayama, Y., Hashimoto, N. and Inoko, H.
Genome diversity in HLA: A new strategy for detection of genetic
polymorphisms in expressed genes within the HLA class III and class
I regions
JOURNAL 2
REFERENCE Unpublished
AUTHORS 2 (bases 1 to 30911)
TITLE Shima, T.
JOURNAL Direct Submission
REFERENCE Submitted (08-JUL-2002) Takashi Shima, Tokai University School of
Medicine, Molecular Life Science 2, Bohseidai, Isehara, Kanagawa
259-1193, Japan (E-mail: tshima@is.icc.u-tokai.ac.jp,
Tel: 81-463-93-1121, Fax: 81-463-94-8884)
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 REFERENCE 1 (sites)
 AUTHORS Shima,T., Tamiya,G., Oka,A., Takishima,N., Yamagata,T.,
 Kikkawa,E., Iwata,K., Tomizawa,M., Okuaki,N., Kuwano,Y.,
 Watanabe,K., Fukuzumi,Y., Itakura,S., Sugawara,C., Ono,A.,
 Yamazaki,M., Tashiro,H., Ando,A., Ikemura,T., Soeda,E., Kimura,M.,
 Bahram,S. and Inoko,H.
 Molecular dynamics of MHC genes unraveled by sequence analysis of
 the 1,796,938-bp HLA class I region
 Proc. Natl. Acad. Sci. U.S.A. 96 (23), 13282-13287 (1999)
 2002/539
 TITLE
 JOURNAL MEDLINE
 PUBMED 10557312
 REFERENCE 2 (bases 1 to 39196)
 AUTHORS Shima,T. and Takishima,N.
 TITLE Direct Submission
 JOURNAL Submitted (29-JUN-1999) Takashi Shima, Tokai University School of
 Medicine, Department of Molecular Life Science 2, Bohseidai,
 Isehara, Kanagawa 259-1193, Japan
 (E-mail:tsushima@is.tokai.ac.jp, Tel:81-463-93-1121,
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AUTHORS Sycamore, N.
 TITLE Direct Submission
 JOURNAL Submitted (23-APR-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: clonerequest@sanger.ac.uk

COMMENT

On Apr 7, 2002 this sequence request replaced g1:19309560.
 During difference assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em, EMBL; Sw, SWISSPROT; Tr, TrEMBL; Wp, WORMPEP; information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep XXbac-34D1 is from a CHORI-502 human bac - COX cell line library VECTOR: pTARBAC2.1

This sequence was generated from part of bacterial clone contigs constructed by the MHC Haplotype Consortium and collaborators. Further information can be found at <http://www.sanger.ac.uk/HGP/Chr/MHC>.

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 QY 715 CTTGCTTCAGAGGCTTCGAGCCCACTTACCTCCACCCGGTCTTCTGCCCCGCGATCG 774
 Db 67126 CTTGCTTCAGAGGCTTCGAGCCCACTTACCTCCACCCGGTCTTCTGCCCCGCGATCG 67067
 QY 775 CTGGGAGAGGCTATGATGATGTTCTTCTTCTGCACTGTTGGCGGGGAGAGAACT 834
 Db 67066 CTGGGAGAGGCTATGATGATGTTCTTCTTCTGCACTGTTGGCGGGGAGAGAACT 67007
 QY 835 ATCAGTAGACAGCTGCTGCTTCATGAAAGGAAAAATAAATCATGTTTCTTAA 891
 Db 67006 ATCAGTAGACAGCTGCTGCTTCATGAAAGGAAAAATAAATCATGTTTCTTAA 66950

RESULT 14
 AP000510 99999 bp DNA linear PRI 22-AUG-2001

LOCUS AP000510 Homo sapiens genomic DNA, chromosome 6p21.3, HLA Class I region,
 DEFINITION Homo sapiens genomic DNA, chromosome 6p21.3, HLA Class I region,
 ACCESSION AP000510 BAO00025
 VERSION AP000510.2 GI:7380878

KEYWORDS
 SOURCE
 ORGANISM

REFERENCE
 AUTHORS Shih, S., Tam, Y. G., Oka, A. and Inoko, H.
 TITLE Homo sapiens 2,229,817bp genomic DNA of 6p21.3 HLA Class I region
 JOURNAL Published Only in Databases (1999)
 REFERENCE 2 (bases 1 to 99999)
 AUTHORS Hirakawa, M., Yamaguchi, H., Imai, K. and Shimada, J.
 TITLE Direct Submission
 JOURNAL Submitted (21-SEP-1999) Mika Hirakawa, Japan Science and Technology Corporation (JST), Advanced Databases Department, 5-3, Yonbancho, Chiyoda-ku, Tokyo 102-0081, Japan (E-mail: mika@tokyo.jst.go.jp, URL: <http://www-alls.tokyo.jst.go.jp/>, Tel: 81-3-5214-8491, Fax: 81-3-5214-8470)
 On Mar 31, 2000 this sequence version replaced g1:5926697.
 This sequence is conducted by Tokai University as a JST sequencing Team.

COMMENT

Principal Investigator: Hidetoshi Inoko Ph.D
 Phone: +81-463-93-1121, Fax: +81-463-94-8884,
 The sequence is submitted by Human Genome Sequencing in ALLIS project of JST
 Japan Science and Technology Corporation (JST)
 5-3, Yonbancho, Chiyoda-ku, Tokyo, 102-0081 Japan
 For further information about this sequences, please visit our
 sequence archive web site (<http://www-alls.tokyo.jst.go.jp/HGS/top.html>) or send email to webmaster@www-alls.tokyo.jst.go.jp
 Sequence updated (28-Mar-2000).

FEATURES

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 2016. 2435
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FSSNPILVSGAASSAIAFPVGTGGVQLCGSGTGKPCSPSSSKVPSSISSSS
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Matches 775;	Conservative 0;	Mismatches 2; Indels 0; Gaps 0;
QY	115	AAGGCAATCTCAGGCGAGGAGGACCCCTCTCAACCCACCGCAGAGACCAGAGAG 174
DB	3766	ACAGGCAATCTCAGGCGAGGAGGACCCCTCTCAACCCACCGCAGAGACCAGAGAG 38225
QY	175	GCAGGCTCCCAACATTCGCTCAGGGGCCCCCAGTCCCGGATACCTTGGCAGAGGCA 234
DB	3826	GCAGGCTCCCAACATTCGCTCAGGGGCCCCCAGTCCCGGATACCTTGGCAGAGGCA 38885
QY	235	CCCCCTCTTTTGAAGATCTTCGCGCTACCCGCGCAGTGTCTCCAGAGACCTGTCT 294
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QY	295	GAAATGGAATGTGGCCCCCTGAACCGGCTGAAGAGATCTCTCTCAACTTCCCGGCT 354
DB	3946	GAAATGGAATGTGGCCCCCTGAACCGGCTGAAGAGATCTCTCTCAACTTCCCGGCT 40055
QY	355	GACGACCCCTTGAGCGGCGAGACCCGACGCCAGAGAAAACCCCTGAGCTCTGACCTGAG 414
DB	4006	GACGACCCCTTGAGCGGCGAGACCCGACGCCAGAGAAAACCCCTGAGCTCTGACCTGAG 40655
QY	415	GTGAGCAACCGAATCTCAGAGAGAGCTAAGACTTAACCCACCCGGGAAAGATACAGATTA 474
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QY	475	TGAGATCCCTCAGCGGCTTCTGTTCCAGGAGATCTCAGGACCAAGCCTCTTCCACCC 534
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DB	4186	TCTGATTCGCCGTAATCTTCCCAATTAGACTTAATCTCTTAAACCTCTTCTCATTC 42455
QY	595	CTCGATTATTTTGAAGCCCGTAAAGGTGATGTTCTCAATATTTCTGCCCCCTCTGAGA 654
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QY	655	TCGATTAATTAATCTCAATCGATCGCCGTTTTTCTCTGACAGACTTAAGCTTAATCTCTTA 714
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QY	715	CTCGAGCTTCAAGGCTCGGCCCACTACCTCCACCCCGGCTTCGAGCCGCGAGATCG 774
DB	4366	CTCGAGCTTCAAGGCTCGGCCCACTACCTCCACCCCGGCTTCGAGCCGCGAGATCG 44255
QY	775	CTGGGGGAGGCTTAATGATCTGTGTTCCCTTCTGACACCTGTGTGGCCGCGAGAGAACT 834
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QY	835	ATCAGTGAACAGCTGCTGCTTCCATGAAGAGAAAAATTAATCATGTTTCTTAA 891
DB	4486	ATCAGTGAACAGCTGCTGCTTCCATGAAGAGAAAAATTAATCATGTTTCTTAA 4542
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LOCUS	BX927139/c	
DEFINITION	Human DNA sequence from clone DAMA-72F24 on chromosome 6, complete	
ACCESSION	BX927139	
VERSION	BX927139.7	
KEYWORDS	GI:48374126	
SOURCE	HTG.	
ORGANISM	Homo sapiens (human)	
	Homo sapiens	
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	

REFERENCE
AUTHORS
TITLE
JOURNAL

1 (bases 1 to 135396)
Phlillimore, B.
Direct Submission
Submitted (06-JUN-2004) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequests@sanger.ac.uk
On Jun 6, 2004 this sequence version replaced gl142734889.
----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk

During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest, except on the rare
occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
Em: EMBL; Sw: SWISSPROT; Tr: TREMBL; Wp: WORMPEP; Information
on the WORMPEP database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
was generated from part of bacterial clone contigs constructed by
the MHC Haplotype Consortium and collaborators. Further information
can be found at
http://www.sanger.ac.uk/HGP/chr6/MHC
DAMA-72F24 is from the DNA-Arts human BAC library MANN.1 VECTOR:
pBelOBAC11.

FEATURES
source

Location/Qualifiers
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/clone="DAMA-72F24"
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ORIGIN

Query Match 86.8%; Score 773.8; DB 9; Length 135396;
Best Local Similarity 99.7%; Pred. No. 8.5e-166;
Matches 775; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 115 AGAGGATCTCAAGGACGAGGACACCCCTCTCAACCCGAGAGGAGAG 174
DB 129845 ACAGGATCTCAAGGACGAGGACACCCCTCTCAACCCGAGAGGAG 129786
QY 175 GCAAGGCTCCCAATGCTCAAGGACCCCACTCCCGGTGACCTTGGCAGGGCA 234
DB 129785 GCAAGGCTCCCAATGCTCAAGGACCCCACTCCCGGTGACCTTGGCAGGGCA 129726
QY 235 CCCCTCTTTGAAGATCTCCGCTACCGCCCACTGCTCTGAGAGACTGCT 294
DB 129725 CCCCTCTTTGAAGATCTCCGCTACCGCCCACTGCTCTGAGAGACTGCT 129666
QY 295 GAAACTGAGTGTGCTCCCTGAAACGCTGAAACGAGTCTCTCAACTCCCGGCT 354
DB 129665 GAAACTGAGTGTGCTCCCTGAAACGCTGAAACGAGTCTCTCAACTCCCGGCT 129606
QY 355 GACGACCTTGGCGGAGAGACCCCAAGCCCAAGAAAACCTTGGCTCTGAG 414
DB 129605 GACGACCTTGGCGGAGAGACCCCAAGCCCAAGAAAACCTTGGCTCTGAG 129546
QY 415 GTGAGCAACGACCTCAAGAGAGCAGACTTAGACCAACCCCGGAGAGTACAGATA 474

DB 129545 GTGAGCAACGACCTCAAGAGAGCAGACTTAGACCAACCCCGGAGAGTACAGATA 129486
QY 475 TGAAGTCCCTCAAGCCGTTGTTCCAGGACATCTCCAGGACCCCTCTCCACC 534
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QY 535 TCGATTCCCGGGAATTCTCCCAATTGACCTATCTCTTAAACCTTCCCTCATTC 594
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DB 129365 CTCGGTTTATTCGAACCCGTAAAGTGTGTTCTCAATATTTCTGTCCCTCTGAGA 129306
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DB 129125 ATCAGTGAACAGCTGCTGCTTCCATGAAACGAAAAATTAATCATGTTTCTTA 129069

Search completed: January 11, 2005, 08:16:02
Job time : 4040 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 11, 2005, 06:51:45 ; Search time 3417 Seconds
(without alignments)
9501.844 Million cell updates/sec

Title: US-09-994-365-1

Perfect score: 891
Sequence: 1 ccccttgggggtcccgagca.....taaatcatgttctta 891

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%
Listing first 45 summaries

Database :

EST:*
1: gb_esc1:*
2: gb_esc2:*
3: gb_esc3:*
4: gb_esc4:*
5: gb_esc5:*
6: gb_esc6:*
7: gb_esc7:*
8: gb_esc8:*
9: gb_esc9:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	408.2	45.8	419	2	BF513178
2	372.2	41.8	634	7	CF764947
3	355.2	39.9	593	7	CF765720
4	323.8	36.3	336	1	A1150762
5	303.6	34.1	383	2	AW315342
6	245.8	27.6	422	1	A1596929
7	244.2	27.4	562	1	AA530301
8	234.8	26.4	451	9	CG484009
9	234.4	26.3	669	9	CG484609
10	233.4	26.2	416	9	CG484452
11	232.4	26.1	243	8	AO357151
12	230.2	25.8	442	9	CG487403
13	212.6	23.9	372	8	AO136453
14	212.4	23.8	475	9	CG473878
15	209.8	23.5	386	9	CG474680
16	202.2	22.7	322	9	CG474695
17	192	21.5	332	1	AA763309
18	179.2	20.1	451	1	AA798896
19	169	19.0	395	9	CG528207
20	167	18.7	283	9	CG474588
21	123.2	13.8	379	1	AA791103
22	119.6	13.4	204	1	AA733661
23	113.6	12.7	489	8	BH098389
24	106	11.9	763	8	AF057073

25	100	11.2	361	1	AA168568
26	86.8	9.7	409	7	CF768607
27	82.4	9.2	494	9	CE197442
28	73.2	8.2	873	9	CL498274
29	72.6	8.1	1129	9	AG448563
30	68.6	7.7	1236	4	BM927210
31	68.4	7.7	1909	9	CL078604
32	67.8	7.6	1073	5	BQ961142
33	65.6	7.4	1297	5	BQ064843
34	65.4	7.3	1703	9	CL078618
35	65	7.3	1094	6	CD509997
36	64.4	7.2	1153	8	CC252982
37	64	7.2	1063	9	CNS040FA
38	63.8	7.2	1406	7	CK408425
39	63.6	7.1	1365	9	CG745655
40	63.2	7.1	1839	9	CG747711
41	62.8	7.0	1299	2	BR455157
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ALIGNMENTS

RESULT 1
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LOCUS
DEFINITION
UI-H-BM1-am]-d-04-0-UI.s1 NCI CGAP Sub7 Homo sapiens cDNA clone
IMAGE:3070111 3', mRNA sequence.
BF513178
BF513178.1 GI:11598357
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 419)
REFERENCE
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
CONTACT: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
The sequence contained an oligo-dT track that was present in the
oligonucleotide that was used to prime the synthesis of first
strand cDNA and therefore this may represent a bonafide poly A
tail. cDNA Library Preparation: M.B. Soares Lab Clone distribution:
NCI-CGAP clone distribution information can be found through the
I.M.A.G.E. Consortium/ILNI at:
www-bio.litl.gov/bdtp/image/image.html
Seq primer: M13 forward
POLYA=yes.

FEATURES

SOURCE

1. 419
/organism="Homo sapiens"
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/db_xref="taxon:9606"
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/lab host="DH10B (Life Technologies)"
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/note="Vector: pMT2D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; NCI CGAP Sub7
is a subcloned library derived from NCI CGAP Sub6. The
NCI CGAP Sub7 library had 12 million recombinants. A
single-stranded DNA preparation of NCI CGAP Sub6 was used
as a tracer in a subtractive hybridization with a diver
comprising: 3682-3683, 3798-3803 (IMAGE Clonetype
3334-3337, 3682-3683, 3798-3803 (IMAGE Clonetype
1322376-1323911, 1456008-1456775, 1500552-1502855);
NCI CGAP Kids pool 1 LHAM 3338-3342, 3722-3725, 3776-3778
(IMAGE Clonetype 1323912-1325831, 1471368-1472903),

1492104-1493255); NCI CGAP Lys pool 1 LHM 3575-3582, 3851-3854 (IMAGE Clonide 1414920-1417991, 1520904-1522439); NCI CGAP GC4 pool 1 LHM 3164-3167, 3716-3720, 3733-3735 (IMAGE Clonide 1257096-1258631, 1469064-1470983, 147592-1476743); NCI CGAP P22 pool 1 LHM 2457-2459, 2758-2759, 3062-3068 (IMAGE Clonide 985608-986759, 1101192-1101959, 1217928-1220615); NCI CGAP Colo pool 1 LHM 2644-2653, 2871-2872 (IMAGE Clonide 1057416-1061255, 1144584-1145351). (6% of the driver population), plus a pool of 3,840 arrayed clones from NCI CGAP Sudi (IMAGE Clonide 2708616-2710535) and NCI CGAP Sudi (IMAGE Clonide 2710536-2712455) (4% of the driver population), plus a pool of 11,136 clones from NCI CGAP Sub3 (IMAGE Clonide 2712456-2723591) (10% of the driver population), plus a pool of 5,472 clones from NCI CGAP Sub4 (IMAGE Clonide 2723592-2729326) (40% of the driver population), plus a pool of 4032 clones from NCI CGAP Sub6 (IMAGE Clonide 2728969-2733190) (40% of the driver population). Subtraction was performed as previously described [Bonaldo, Lennon & Soares (1996): Normalization and Subtraction: Two Approaches To Facilitate Gene Discovery. Genome Research 6, 791-806. TAG_TISUB-covary TAG_LIB=NCI CGAP_Ov18 TAG_SEQ=GCACA"

ORIGIN

Query Match 45.8%; Score 408.2; DB 2; Length 419;
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Matches 410; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 465 GTACAGATATGAGTCCCTCAGCCGTTCTGTTCCAGGATCTCCAGGACCCAGCC 524
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QY 525 CTCCTCCACCCCTGATTTCCCGGATTTCTTCCCAATTTAGCTATCTCTTAAACCTCT 584
DB 359 CTCCTCCACCCCTGATTTCCCGGATTTCTTCCCAATTTAGCTATCTCTTAAACCTCT 300
QY 585 TCTCATATCCCTCGATTTTATTTGAAACCCGTAAGGTGATTTCTCAATTTCTCTGTC 644
DB 299 TCTCATATCCCTCGATTTTATTTGAAACCCGTAAGGTGATTTCTCAATTTCTCTGTC 240
QY 645 CTCCTGATGATCTATGATGCTCAATGCTCCGTTTCTCTGACAGCTTAAACC 704
DB 239 CTCCTGATGATCTATGATGCTCAATGCTCCGTTTCTCTGACAGCTTAAACC 180
QY 705 TACTCTCTACCTGCTCCAGGCTGAGCCCACTCCCACTCCACCCGCTTCTGACC 764
DB 179 TACTCTCTACCTGCTCCAGGCTGAGCCCACTCCCACTCCACCCGCTTCTGACC 120
QY 765 CGGCGATGCTGAGGCGAGGCTATGATGATGATGATGATGATGATGATGATGATGAT 824
DB 119 CGGCGATGCTGAGGCGAGGCTATGATGATGATGATGATGATGATGATGATGATGAT 60
QY 825 GCGAGGATCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 877
DB 59 GCGAGGATCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 7

RESULT 2

CF764947

LOCUS

CF764947 634 bp mRNA linear EST 17-OCT-2003

DEFINITION

CF764947

ACCESSION

CF764947

VERSION

CF764947.1

KEYWORDS

EST

SOURCE

Bos taurus (cow)
Bos taurus
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

REFERENCE
1 (bases 1 to 634)
AUTHORS
Mang, Y.H., McWilliam, S. and Lehnert, S.
TITLE
Transcription profiling of cattle skin
JOURNAL
Unpublished (2003)
CONTACT
Contact: Dr Yonhong Wang
FUNCTIONAL GENOMICS LAB
CSIRO Livestock Industries
Level 5, Queensland Biosciences Precinct, University of Queensland,
306 Carmody Road St. Lucia QLD Australia
Tel: 07 3214 2445
Fax: 07 3214 2685
Email: Yonhong.Wang@csiro.au
Plate: 40 row: G column: 07.
Location/Qualifiers

FEATURES

source

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/lab_host="XJ1-BlueMRF/strain"
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female Hereford-Shorthorn."

ORIGIN

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Best Local Similarity 76.7%; Pred. No. 6.6e-82;
Matches 488; Conservative 0; Mismatches 129; Indels 19; Gaps 2;

QY 56 AACTAGCATGATCTCAACTGAGAGCTCTGGGATCTGATCTCTTGTCTGACACCA 115
DB 2 AGATAGTTAAGATGCTCAACTGAGAGCTCTGGGATCTGATCTCTTGTCTGACACCA 61
QY 116 GAGGCACTCAGGCGAGGCGGCAACCCCTCACCACCCGAGAGAGAGAGAGAGAG 175
DB 62 GAGGCACTCAGGCGAGGCGGCAACCCCTCACCACCCGAGAGAGAGAGAGAGAGAG 121
QY 176 CAGGCTCCCCAATCTGCTCAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 235
DB 122 AGGCGGCTCCACATCTGCTCAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 181
QY 236 CCGCTCTTTTGAATCTCTGCTCAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 295
DB 182 CCGCTCTTTTGAATCTCTGCTCAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 241
QY 296 AAATGAGATCTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 355
DB 242 AAATGAGATCTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 301
QY 356 ACAGCCCTTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 415
DB 302 ACAGCCCTTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 361
QY 416 TGAACACCGACTCAGATAT 475
DB 362 TGAACACCGACTCAGATAT 421
QY 476 GAGATCCCTCAGCGCTCTGTTCCAGGCACTCCAGGCACTCCAGGCACTCCAGGCACTCC 535
DB 422 GAGATCCCTCAGCGCTCTGTTCCAGGCACTCCAGGCACTCCAGGCACTCCAGGCACTCC 472
QY 536 CTGATCCCTCAGGATCTTCCCAATTTAGCTATCTCTTAAACCTTCTCTCTCAATTTCC 595
DB 473 CTGATCCCTCAGGATCTTCCCAATTTAGCTATCTCTTAAACCTTCTCTCTCAATTTCC 532
QY 536 TCGGTTTATTTGAACCGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 655

[illegible]

Oy	370	GCAGAGCCCGAGCCCCCAGAAAAACCCCTGGCCTCTGACCTGTAGAGTGACAAACGACCT	429
Db	316	GCAAGACCCCAAGCTCCAGAAAAACCCCTGGCCACTGCTCCCTGAGGTGAGACAGAGATCT	375
Oy	430	CAGAGAGGCCAGACTTAGACCCACCCCGGAGAGTACAGATATATGAGTCCCTCAGC	489
Db	376	CACAGAGAGCCAGACTTTGACCCACCCAGGAGAGATACAGATTAACGGCCCCCAGAGGC	435
Oy	490	CGTTCTGTCCCAAGCAATCTCAGGAAACCCAGCGCCCTCCACACCTCTGATATCCCGGGA	549
Db	436	-----ATCTGGACTTCTGCTCTCAAAACATCTTAACCTTTGATTTCCCTTGA	486
Oy	550	ATTCTCCCAATTTAGCGCTATCTCTTAAACCTTTCTCAATTCCTCGGTTTAAATCTG	609
Db	487	ATTCTCCCAATTTAGCTTAACCTCTTAATCTTTCTCAATTCCTCAAGTTTAAATCTG	546
Oy	610	AACCCGTAAAGTGTGTCTTCATATTTCTCTGCCCCCTCTGAGATGCATACCTTA	664
Db	547	AA-----GATTTGTGCATATTTCTGTCCTCCCTCTGGAATCGGAATTTA	591

	RESULT 4
A1150762/c	
LOCUS	336 bp mRNA linear EST 30-SEP-1998
DEFINITION	GQ060904.xl Soares_fetal_heart_NDHLH19W Homo sapiens cDNA clone IMAGE:11708830 3 , mRNA Sequence.
ACCESSION	A1150762
VERSION	A1150762.1 GI:3679231
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap .
AUTHORS	Tumor Gene Index
TITLE	Unpublished (1997)
JOURNAL	Contact: Robert Strausberg, Ph.D. Email: cgapps@omni.nih.gov
COMMENT	This clone is available royalty-free through LNL ; contact the IMAGE Consortium (info@image.lnl.gov) for further information. Seq primer: -40mU3 fwd. ET from Amersham High quality sequence stop: 315.

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FEATURES
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        Location/Qualifiers
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                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone="IMAGE:1708830"
                /sex="unknown"
                /dev_stage="19 weeks"
                /lab_host="DH10B (ampicillin resistant)"
                /clone_lib="Soares fetal heart NBH19W"
                /note="Organ: heart; Vector: pT73D (Pharmacia) with a
                modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
                strand cDNA was primed with a Not I - oligo(dT) primer [5'
                TGTTACCAATCTGAAGTGGAGGCCGACATCTTTTCTTTTCTTTT 3'],
                double-stranded cDNA was size selected, ligated to Eco RI
                adapters (Pharmacia), digested with Not I and cloned into
                the Not I and Eco RI sites of a modified pT73 vector
                (Pharmacia). Library went through one round of
                normalization to a Cot = 5. Library constructed by
                M.Patima Bonaldo. This library was constructed from the
                same fetus as the fetal lung library, Soares fetal lung
                NBH19W."

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Query Match	36.34;	Score 323.8;	DB 1;	Length 336;
Best Local Similarity	97.94;	Pred. No. 7.1e-70;		
Matches 328;	Conservative 0;	Mismatches 7;	Indels 0;	Gaps 0;

QY	557	CCAATTGAGCCGATCTCCCTTAAACGCTCCGATTCCTCCGAGTTTATCTGAACCGGT	616
Db	336	CCAAATTGAGCGATTTCTCTTAAACCTTTTCCCTCATTCCTCCGAGTTTATTTGAACCGGT	277
QY	617	AAGGTGGTGTCTCAATATTTTCTGTCCCTCCCTGAGATCCATTAAGTCTCTCAATCG	676
Db	276	AAGGTGGTGTCTCAATATTTTCTGTCCCTCCCTGAGATCCATTAAGTCTCTCAATCG	217
QY	677	CCCGTTTTTTCCTCTGACAGCCTTAAGGCTACTCTCTCACTGAGCCGACGAGCCTGAGGCC	736
Db	216	CCCGTTTTTTCCTCTGACAGCCTTAAGGCTACTCTCTCACTGAGCCGACGAGCCTGAGGCC	157
QY	737	CACCGAAGTCCCAAGCCGCTTCTCTGCGCGGCGCATTCGTGGGGCAGGGCTATGTGACTG	796
Db	156	CACCTACTCCCAAGCCGCTTCTCTGCGCGGCGCATTCGTGGGGCAGGGCTATCGTACTG	97
QY	797	TGTTCCCTTCTGCACTGATGGCCGGCGGCGAGAACTATCAGTAGACAGCTGCTGCTTC	856
Db	96	TGTTCCCTTCTGCACTGATGGCCGGCGGCGAGAACTATCAGTAGACAGCTGCTGCTTC	37
QY	857	CATGAACGGGAAAAATATAAATCAGTTTTCTTAA	891
Db	36	CATTAACCCAAAAATATAAATCAGTTTTCTTAA	2

RESULT 5	LOCUS	DEFINITION	VERSION	KEYWORDS	SOURCE	EST
AW315342	AW315342	12593 MARC 2P1G Sus scrofa CDNA 5', mRNA sequence.	AW315342	GI:6744598	Sus scrofa (pig)	EST 09-JUL-2000

REFERENCE
AUTHORS
1 (bases 1 to 383)
Fahrenkrug, S.C., Smith, T.P.L., Freking, B.A., Cho, J., White, J.,

TITLE	Porcine gene discovery by normalized cDNA-library sequencing and EST cluster assembly
JOURNAL	Mamm. Genome 13 (8), 475-478 (2002)
MEDLINE	22213789
PUBMED	12226715
COMMENT	Contact: Smith TPL

COMMENT:
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smilt@email.marc.usda.gov
Single pass sequencing. Bases called and trimmed with phred
v0.980904.e. Vector identified by cross_match with the -mnscore 20
and -mismatch 12 options.
PCR Primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCCAGTCACGACG
plate: 8 row: A column: 14
Seq primer: ATTAGCTGACACTAATG.
Location/Qualifiers
1. 383

ORIGIN

Query Match

34.18; Score 303.6; DB 2; Length 383;

	Best Local Similarity, 87.2%;	Pred. No. 7,9e-65;	
Matches 333;	Conservative 0;	Mismatches 49;	Indels 0; Gaps 0
QY	75 CTGGAAGCTCCTGGGGATCTGTGTCCTTTGCTGCAACAGAGGATCTAGGAGCGA	134	
Db	2 CTGGAAGCTACTGGGAGATCTGTGTCCTTTGCTGTCGCCGAGGATCTCAGGACGG	61	
QY	135 GGGCCACCCCTCTACCCCAACCCGAGAGAGACGAGAGAGCGAGCTCCCAATTGCC	194	
Db	62 AACCACCCATCTCCCCATCCACGAGAGGCTTCAGAGAGAGAGGGCTCCCAACTGCC	121	
QY	195 TCAGGGACCCCGCAGTCCCGGAGACCTTGGCCAGGGGACCCCTCTTTGAAGATCC	254	
Db	122 TCGGGGGCCCCCAATCCCGGTGACCTTTGGCCAGGGTACTCTCTAATCTTTGAGACC	181	
QY	255 TCCGCGTACCCGCCCCAGTGTCTCCCTGAGAGACCTGTGCTGAAACTGTGGCCCC	314	
Db	182 TCCAGCTCCAGGGGCCCAATCGTCCTGAGAGACCTGTGTAATCTGGAAGTCTGGCTCC	241	
QY	315 TGAACCGCTTGAAACGATCTCTCTCAACTCTCCCGGCTTACGACACCTTGGCGGAGG	374	
Db	242 TGAACCCCTCTGTACTGATCTCCCTCTCAACTCCCGGCTGACGACCCCTGGCAGAGG	301	
QY	375 ACCCAGCGCCCGAGAAAACCCCTGGCTCTCTGCCCTCTGAGGTGAGCAACGACTCMAGA	434	
Db	302 ACCCAGCTTCAGAAAACCCCTGGCCACTGCCCCCTGAGGTGAGCACGAGTCCGAGA	361	
QY	435 GAGCGAGACTTAGACCAACC 456		
Db	362 GAGCGAGACTTAGACCAACC 383		

[illegible]

Email: mouseest@watson.wustl.edu
This clone is available royalty-free through ILM, / contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:537028
This read is a RESEQUENCE of a previously sequenced mouse clone
This read has been verified (found to hit its original self in the
correct orientation)
Seq primer: -40RP from Gibco
High quality sequence STOP: 396.
Location/Qualifiers
1..422
source

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/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:932108"

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/sex="females"
/tissue type="whole skin"
/dev stage="11 weeks old"
/lab_host="SOLR (kanamycin resistant)"
/clone_lib="Stratagene mouse skin (#937313)"
/notes="Organ: skin; Vector: pBluescript SK-; Site: 1:
ECORI; Site 2: XhoI; Cloned unidirectionally. Primer:
Oligo dt. Whole skin from 11 week old C57BL/6 female mice.
Average insert size: 1.0 kb; Uni-ZAP XR Vector: -5'
adaptor sequence: 5' GAATTCGCGACGAG 3' -3' adaptor
sequence: 5' CTCGAGTTTCTTTTCTTTT 3'."

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ORIGIN

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Query Match      27.6%; Score 245.8; DB 1; Length 422;
Best Local Similarity 79.2%; Pred. No. 2.1e-50;
Matches 305; Conservative 0; Mismatches 77; Indels 3; Gaps 1;

Qy 94 CTGGTCTCTTGGCTGACACCGAGAGCATCTCAGCGAGGAGCCCTCTCAGCCA 153
Db 2 CTGGTCTCTTGGCTGATGAGAGGATTTCAAGCA--ATGGCGACCTTCTCCGGA 58
Qy 154 CCGCGAGAGACCGAGAGGAGGAGGCTCCCAATTGCTCAGGGGCCCCAGTCCC 213
Db 59 TCTACAGACACCGACGAGAGAGAGACTCCACATTGCTCTGGAGACCCCAATCCT 118
Qy 214 GGTGACCTTGGCCAGGAGGACCCCTCTCTTGAAGATCTCGGCTTACCGCCAGT 273
Db 119 GGTGATCTCTGGCTGAGGAGGCTCTCTTGTGTATGAACTTCGGCTCCAGGCTCAAC 178
Qy 274 GGTCTCTGAGAGACCTGCTCTGAACTGAGTCTGGCCCTTGAACCGCTTGAACGAT 333
Db 179 GGTCTCTGAGAGATCTTCTGACAGTGTCTGAGCCCAAGCCCAAGACATGAT 238
Qy 334 CTCTCTCAACTCCCGGCTTGAAGACCTTGGCCGAGAGACCCCAAGCCCAAGAAC 393
Db 239 CCGCTTAACTCTCTGCTGATGACCTTGGCCGAGAGACCCCAAGCCCAAGAAC 298
Qy 394 CCGTGGCTCTGCTGCTGAGTGAACACCGACTTGAAGAGAGAGAGAGAGAGAGAG 453
Db 299 CCGTGGCTCTGCTGCTGATGAGACCTTGAAGAGAGAGAGAGAGAGAGAGAGAG 358
Qy 454 CCGCGGAGAGATACAGATTAATGA 478
Db 359 CCGCGGAGAGATTAATGAAGGA 383

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RESULT 7      562 bp      mRNA      linear      EST 22-JUL-1997
AA530301      vJ46e1.r1 Stratagene mouse skin (#937313) Mus musculus cDNA clone
LOCUS         vJ46e1.r1 Stratagene mouse skin (#937313) Mus musculus cDNA clone
DEFINITION    AA530301.1 GI:2273007
VERSION       AA530301.1 GI:2273007
KEYWORDS      EST.
SOURCE        Mus musculus (house mouse)
ORGANISM      Mus musculus
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
               1 (bases 1 to 562)
REFERENCE     1 (bases 1 to 562)
AUTHORS      Mairia, M., Haller, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
               Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
               Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
               Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
               Waterston, R.
               The Mashu-HMI Mouse EST Project
               Unpublished (1996)
               Contact: Marra M/Mouse EST Project
               Mashu-HMI Mouse EST Project
               Washington University School of Medicine
               4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
               Tel: 314 286 1800
               Fax: 314 286 1810
               Email: mouseest@watson.wustl.edu

```

This clone is available royalty-free through LML; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MG1:537028

Seq primer: -28m13 rev1 ET from Amersham

High quality sequence stop: 221.

Location/Qualifiers

FEATURES

source

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1. 562
/organism="Mus musculus"
/mol type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:932108"
/sex="females"
/tissue type="whole skin"
/dev stage="11 weeks old"
/lab_host="SOLR (kanamycin resistant)"
/clone_lib="Stratagene mouse skin (#937313)"
/notes="Organ: skin; Vector: pBluescript SK-; Site: 1:
ECORI; Site 2: XhoI; Cloned unidirectionally. Primer:
Oligo dt. Whole skin from 11 week old C57BL/6 female mice.
Average insert size: 1.0 kb; Uni-ZAP XR Vector: -5'
adaptor sequence: 5' GAATTCGCGACGAG 3' -3' adaptor
sequence: 5' CTCGAGTTTCTTTTCTTTT 3'."

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ORIGIN

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Query Match      27.4%; Score 244.2; DB 1; Length 562;
Best Local Similarity 79.0%; Pred. No. 5.6e-50;
Matches 304; Conservative 0; Mismatches 78; Indels 3; Gaps 1;

Qy 94 CTGGTCTCTTGGCTGACACCGAGGATCTCAGCGAGGAGCCCTCTCAGCCA 153
Db 1 CTGGTCTCTTGGCTGATGAGAGGATTTCAAGCA--ATGGCGACCTTCTCCGGA 57
Qy 154 CCGCGAGAGACCGAGAGGAGGAGGCTCCCAATTGCTCAGGGGCCCCAGTCCC 213
Db 58 TCTACAGACACCGACGAGAGAGAGACTCCCAATTGCTCTGGAGACCCCAATCCT 117
Qy 214 GGTGACCTTGGCCAGGAGGACCCCTCTCTTGAAGATCTCGGCTTACCGCCAGT 273
Db 118 GGTGATCTCTGGCTGAGGAGGCTCTCTTGTGTATGAACTTCGGCTCCAGGCTCAAC 177
Qy 274 GGTCTCTGAGAGACCTGCTCTGAACTGAGTCTGGCCCTTGAACCGCTTGAACGAT 333
Db 178 GGTCTCTGAGAGATCTTCTGACAGTGTGCTGGCCCAAGCCCAAGCACTGAT 237
Qy 334 CTCTCTCAACTCCCGGCTTGAAGACCTTGGCCGAGAGACCCCAAGCCCAAGAAC 393
Db 238 CCGCTTAACTCTCTGCTGATGACCTTGGCCGAGAGACCCCAAGCCCAAGAAC 297
Qy 394 CCGTGGCTCTGCTGCTGAGTGAACACCGACTTGAAGAGAGAGAGAGAGAGAGAG 453
Db 298 CCGTGGCTCTGCTGCTGATGAGACCTTGAAGAGAGAGAGAGAGAGAGAGAGAG 357
Qy 454 CCGCGGAGAGATACAGATTAATGA 478
Db 358 ACCGAGAGAGATTAATGAAGGA 382

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RESULT 8      451 bp      DNA      linear      GSS 01-OCT-2003
CG484009      G8T17807 Mus musculus 129Sv/Ev Mus musculus genomic clone G8T17807,
LOCUS         G8T17807 Mus musculus 129Sv/Ev Mus musculus genomic clone G8T17807,
DEFINITION    CG484009.1 GI:3729343
VERSION       CG484009.1 GI:3729343
KEYWORDS      GSS.
SOURCE        Mus musculus (house mouse)
ORGANISM      Mus musculus
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
               1 (bases 1 to 451)
REFERENCE     1 (bases 1 to 451)
AUTHORS      Zambrowicz, B.P., Abuin, A., Ramirez-Solis, R., Richter, L.J.,
               Piggett, J., Beltrandeirio, H., Buxton, E.C., Edwards, J., Finch, R.A.,

```


TITLE	JOURNAL
COMMENT	OmitBank Lexicon Genetics Incorporated 4000 Research Forest Drive, The Woodlands, TX 77381, USA Email: material@lexgen.com Gene trap sequence tag generated by 3' RACE from mouse ES cells as described in Zambrowicz et al (Nature, 1998 Apr 9;392(6676):608-11) Class: Gene Trap. Location/Qualifiers 1..416 /organism="Mus musculus" /mol_type="genomic DNA" /strain="129Sv/Ev" /db_xref="taxon:10090" /clone="OST13885" /cell_type="embryonic stem cell" /clone_lib="Mus musculus 129Sv/Ev"
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Query Match	26.2%; Score 233.4; DB 9; Length 416;
Best Local Similarity	79.3%; Pred.No. 2.6e-47;
Matches 276; Conservative	0; Mismatches 72; Indels 0; Gaps 0;
Dy	131 GCGAGGGCCACCCCTTCAACCACCCGAGAGACCGAGAGAGCAGAGCTCCCCAAT 190
Dy	9 GCAATGGGAGCCCTTCNCGGATTYACAGACCCACAGAAAGAGAGACTCCACCAT 68
Dy	191 TGCCCTCAGAGGCCCCGAGTCCCGGTGAACCTTGSCAGAGGAGCACCCCTCTTTGAAG 250
Dy	69 TGCCTTGGAGCCCCCAATCCTGTGATTCCTTGACCTGGGCGCTCTTTGTTATG 128
Dy	251 ATCTCCGCTTAACCGCCAGTCGTCTCTGGAGAGACTGCTGMACTGGAGTCTGGC 310
Dy	129 AACCTCGGCTTCGAGGCTCAACGCTCCTGGAGAGATCTTCTGACAGTGGTCTGGC 188
Dy	311 CCCCTGAACCGCTTGAAGCGATCTCTCAACTCTCCCGGCTTAGCAGACCTTTGGCCGG 370
Dy	189 CCCCAGAACCCCCCAAGCACTGATCCCCCTTAAACCTCTCTGCTGATGACCCCTGGCCAG 248
Dy	371 CAGAACCCGACCCCCCAGAAAAACCCCTGGCTCTGCCCCCTGAGGTGAGCAACGACCTC 430
Dy	249 CAGGAACCCGACCCCCCAGAAAAACCCCTGGCTCTGAGGTGAGCACTGATCTC 308
Dy	431 AGAGGAGACCGACCTTAGACCCACCCCGGAGAAGTAGATAGATTAATGGA 478
Dy	309 AGGAGGACCGACGACTTGAACCCACCCGAGAAAGATATAGTAGGGA 356
RESULT 11	
AQ357151/c	243 bp DNA linear GSS 24-JAN-1999
LOCUS	CITBI-EI-2534O14.TF CITBI-EI Homo sapiens genomic clone 2534O14,
DEFINITION	genomic survey sequence.
ACCESSION	AQ357151
KEYWORDS	AQ357151.1 GI:4184324
SOURCE	GSS.
ORGANISM	Homo sapiens (human)
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS	Zhao,S., Adams,M.D., Nierman,W., Malek,J., Shizuya,H., Simon,M. and Venter J.C.
TITLE	Use of BAC End Sequences from Caltech Libraries for Sequence-Ready Map Building

JOURNAL
 COMMENT
 Unpublished (1997)
 Other GSSs: C17B1-E1-2534014.TR
 Contact: Shaying Zhao, William Nierman, Mark Adams
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: hbe@tigr.org
 Clones are available from Research Genetics (info@reagen.com). BAC
 end_search page:
http://www.tigr.org/tcd/humgen/bac_end_search/bac_end_search.html.
 Seq primer: M13-21
 Class: BAC ends.

FEATURES
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 Location/Qualifiers
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 /note="Vector: pGelBAC11; Site_1: EcoRI; Site_2: EcoRI;
 Caltech Human BAC Library D"

ORIGIN
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 Best Local Similarity 97.5%; Pred. No. 4,36-47;
 Matches 236; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY	300	TGAGAGTCGGCCCCCTTGAAACCCGCTTAGAACCGATCTCTTAACCTCCCGGCTTGACGA	359
Db	243	TGGAGTCGGGCCCATGAAACGGCTTAGAACGATCTCTTAACCTCCCGGCTTGACGA	184
QY	360	CCCTTGGCGGGCAGAGACCCCAAGCCCAAGAAAACCTTGAGCTCTCTGCGCCCTGAGATGGA	419
Db	183	CCCTTGGCGGGCAGAGACCCCAAGCCCAAGAAAACCTTGAGCTCTCTGCGCCCTGAGATGGA	124
QY	420	CAACCGACTTCAGAGAGAGCCAGACCTAGACCAACCCCGGAGAGATACAGATATATGAG	479
Db	123	CAACCGACTTCAGAGAGAGCCAGACCTAGACCAACCCCGGAGAGATACAGATATATGAG	64
QY	480	TCCCTCAGACCGCTTCTGTTCACAGGCATCTTCAGAGACCAACCGCCCTCTCCACCTCTGA	539
Db	63	TCCCTCAGAAAATCTGTTCACAGGCATCTTCAGAGACCAACCGCCCTCTCCACCTCTGA	4
QY	540	TT 541	
Db	3	TT 2	

RESULT 12
 CGA87403 442 bp DNA linear GSS 01-OCT-2003
 LOCUS
 DEFINITION OST22893 Mus musculus 1295V/5V Mus musculus genomic clone OST22893,
 genomic survey sequence.
 ACCESSION
 CGA87403
 VERSION
 CGA87403.1 GI:37246315
 KEYWORDS
 GSS.
 SOURCE
 Mus musculus (house mouse)
 ORGANISM
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 442)
 Zambrowicz,B.P., Abuin,A., Ramirez-Solis,R., Richter,L.J.,
 Piggett,U., Beltrandeiro,H., Buxton,E.C., Edwards,J., Finch,R.A.,
 Friddele,C.J., Gupta,A., Hansen,G., Hu,Y., Huang,W., Jang,C.,
 Key,B.W., Jr., Klipp,P., Kohlhauff,B., Ma,Z.-Q., Markesich,D.,
 Payne,R., Porter,D.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.-Z.,
 Sparks,M.J., Van Sligtenhorst,I., Vogel,P., Walke,W., Xu,N.,
 Zhu,Q., Person,C., and Sands,A.T.
 Mtl1 kinase deficiency lowers blood pressure in mice: a gene-trap

REFERENCE
 AUTHORS

TITLE
 Mtl1 kinase deficiency lowers blood pressure in mice: a gene-trap

High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 3040 row: L column: 6
Class: BAC ends
High quality sequence scop: 372.
Location/Qualifiers
1. 372
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="Plate:3040 Col:6 Row=L"
/sex="male"
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/note="Organ: sperm; Vector: pBeloBAC11, BAC Clones in E-Coli DH10B"

23.9%; Score 212.6; DB 8; Length 372;
1 Similarity 97.0%; Pred. No. 4e-42;
226; Conservative 0; Mismatches 6; Indels 1; Gaps 1

1 TACTTAGTCTCAGATCGCCCGCTTTTTCCTGTGACAGCCTAAGCCTACTCTCTCACTC 718
1 TACTTAGTCTCAGATCGCCCGCTTTTTCCTGTGACAGCCTAAGCCTACTCTCTCACTC 60

19 GCCTCCAGGCTCGGGCCCACTCACTCCACCCGGTCTTCTGCCCCGGATCGCTGG 778
61 GCTCCAGGCTCGGGCCCACTCACTCCACCCGGTCTTCTGCCCCGGATCGCTGG 120

179 GGCAGAGGCTATGATCTATGTGTCTTCCTTCTGCACTGCGCGGCGGAGAGAACTATCA 838
21 GGCAGAGGCTATGATCTATGTGTCTTCCTTCTGCACTGCGCGGCGGAGAGAACTATCA 180

339 GTAGACAGCTGCTGCTTCATATGAAACGAAAAATATAAATCATGTCTTTCTTAA 891
81 GTAGACAGCTGCTGCTTCATATGAAACGAAAAA-AAAATCATGTCTTTCTTAA 232

CG473878 475 bp DNA linear GSS 01-OCT-2000
OST1668 Mus musculus 129Sv/Ev Mus musculus genomic clone OST1668,
genomic survey sequence.
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CG473878.1 GI:37224767
GSS.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 475)

Zambrowicz, B.P., Abuin, A., Ramirez-Solis, R., Richer, L.U.,
Pigott, J., BeltrandelRio, H., Buckton, E.C., Edwards, J., Finch, R.A.,
Fridde, C.U., Gupta, A., Hansen, G., Hu, Y., Huang, W., Jai, C.,
Key, B.W., Jr., Kip, P., Kohlhauf, B., Ma, Z.-Q., Markesich, D.,
Payne, R., Potter, D.G., Qian, N., Shaw, J., Schrick, J., Shi, Z.-Z.,
Sparks, M.J., Van Sligtenhorst, I., Vogel, P., Walke, W., Xu, N.,
Zhu, Q., Person, C. and Sands, A.T.
Mnk1 kinase deficiency lowers blood pressure in mice: a gene-trap
screen to identify potential targets for therapeutic intervention
Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
Contact: Zambrowicz BP
OmiBank
Lexicon Genetics Incorporated
4000 Research Forest Drive, The Woodlands, TX 77381, USA
Email: materials@lexgen.com
Gene trap sequence tag generated by 3' RACE from mouse ES cells as
described in Zambrowicz et al (Nature, 1998 Apr 9;392(6676):608-1111)

FEATURES	Class:	Gene Trap.
SOURCE	Location/Qualifiers	
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	/clone_11b="Mus musculus 129Sv/Ev"	
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Best Local Similarity	76.9% Pred No. 4.6e-42	
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Dn	129 CAGGAGGGGACCCCTCTCAACCACCGCAGAGAGACCGAGAGGAGGAGGAGGCTCCCCAAC	188
Oy	7 CAGGCAATGGGACCTTCTCCCGATTCACAGACGCCACGAAAAG-AGATCCCAC	65
Dn	189 ATTGCCTCAGGGCCCCCGCATGTCCCGGTGACCCCTTGCCAGAGGCACCCCCTCTTTTGA	248
Oy	66 ATTCGCTCTGGAGACCCCAATCCCTGGATGATCCCTGGGCGGCTCTTGTATTGA	125
Dn	249 AGATCTCCGCGCTACCCGCGCCGACGTCGTCCTGGAGAGACTGCTGAACTGAGATCTG	308
Oy	126 TGAACCTCTCGCTCAGGCTCACCGTCCCTGGAGAATCTTCTTGACAGTGTCCTG	185
Dn	309 GCCCCTTGAAACCGCTTAAGACGATCTCTCAACTCCCGGCTGACGACCTTTGGCC	368
Oy	186 GCCCCCAAAGCCCCAAGCATGATCCCTCTAAACTCTCTGCTGATGACCCCTGGCC	245
Dn	369 GGCAAGACCCAGCCCCCAAAAAACCTTGCTCTCTGCCCCCTGAGTGAGCAACCGAC	428
Oy	246 AGCAAGAACCCAGCCCCCANAAAAACCTTGCTCTCTGCCCCCTGAAATGACATGATC	305
Dn	429 TCAGAGAGAGCCAGACCTTAGACCCACCCCGGAAAGATACGATATGGA	478
Oy	306 TCAGAGAGAGCCANACTTGAACCCACCCAGAAAATAATATATGAGGA	355
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LOCUS CG474680	386 bp DNA linear GSS 01-OCT-2003	
DEFINITION OSR2720 Mus musculus 129Sv/Ev Mus musculus genomic clone OSR2720,		
ACCESSION CG474680	genomic survey sequence.	
VERSION CG474680.1 GI:37225569		
KEYWORDS GSS.		
SOURCE Mus musculus (house mouse)		
ORGANISM Mus musculus		
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS Mamalita; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
1 (bases 1 to 386)		
Zambrowicz,B.P., Abulin,A., Ramirez-Solis,R., Richter,L.V.J.,		
Piggott,J., Beltrando-Rio,H., Buxton,E.C., Edwards,J., Finch,R.A.,		
Friedle,C.J., Gupta,A., Hansen,G., Hu,Y., Huang,W., Jaing,C.,		
Key,B.W., Jr., Kipp,P., Konhanff,B., Ma,Z.-Q., Markesich,D.,		
Payne,R., Porter,D.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.-Z.,		
Sparke,M.J., Van Sigtendorf,I., Vogel,P., Walke,W., Xu,N.,		
Zhu,Q., Person,C., and Sande,A.T.		
Mutl kinase deficiency lowers blood pressure in mice: a gene-trap		
screen to identify potential targets for therapeutic intervention		
Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)		
Contact: Zambrowicz BP		
OmniBank		
Lexicon Genetics Incorporated		
4000 Research Forest Drive, The Woodlands, TX 77381, USA		
Email: material@lexgen.com		
Gene trap sequence tag generated by 3' RACE from mouse ES cells as		
described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)		
Class: Gene Trap.		
Location/Qualifiers		
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/organism="Mus musculus"		
/mol_type="genomic DNA"		
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/clone="OSR1668"		
/cell_type="embryonic stem cell"		
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	1..386	
	/organism="Mus musculus"	
	/mol_type="genomic DNA"	
	/strain="129SV/Ev"	
	/db_xref="taxon:10090"	
	/clone="OSI7270"	
	/cell_type="embryonic stem cell"	
	/clone_1ib="Mus musculus 129SV/Ev"	
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Query Match	23.5%; Score 209.8; DB 9; Length 386;	
Best Local Similarity	74.9%; Pred. No. 2e-41;	
Matches 256; Conservative	0; Mismatches 86; Indels 0; Gaps 0	
Oy	137 GCCACCCCTCTCAACCACCCGAGAGAACCGAGAGAGGCGGTCCCCCATTGGCTTC	196
Db	2 GGCAGACTTCTCCGGATCTACAGACACCCACAATAAAGAGAGACTCCCACCATTTGCCCTC	61
Oy	197 AGGGCCCCCAGTCCCCGGTGACCTTTGGCCAGGGGCAACCCCTCTCTTGAAGAATCCTC	256
Db	62 TGGAGCCCCCATCCCTGGTAATCTGACCTGGGGCGCCTCTTTGTTGATNAACCTTC	121
Oy	257 GCACCAACCGGCCCCAGTGGTCCCTGGAAGACCTCTCTGAAACTGGAAGTCTGACCCCTG	316
Db	122 CGCTTCAGGGCTCCAAACCTCTCTGGANAGATCTTCTCTGACANTGCTGCCCCCAA	181
Oy	317 AACGGCTTAGAACGATCTCTCTCAACTCTCCCGGCTGACGACCCCTTGGCCGGCAGAC	376
Db	182 AGCCCCCNAAGNCATGATCTCCCTTAACCTCTCTCTCNATNAACCCCTGGCCAGCAGAA	241
Oy	377 CCCAGCCCCCAGAAAACCCCTGGCTCTCTGGCCCTTGAGGTGACAACGACTCAGGAG	436
Db	242 CCGANCCCCCAAAAAACCCCTGGCTCTCTGGCCCTCGAATATGACCATGATCTCAGGAG	301
Oy	437 AGCGAGACTGACCCACCCCGGGAGAGTCAAGTAATGGA	478
Db	302 AGCCAACCTTGACCCNCCCAAGAAAATTATAATTAGGGA	343

Search completed: January 11, 2005, 09:13:06
Job time : 3423 secs

FEATURES

Location/Qualifiers

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 11, 2005, 09:15:10 ; Search time 111 Seconds
(without alignments)

5705.522 Million cell updates/sec

Title: US-09-994-365-1

Perfect score: 891

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Scoring table: OLIGO_NIC

Gapop 60.0 , Gapext 60.0

Searched: 824507 seqs, 355394441 residues

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Minimum DB seq length: 0

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Post-processing: Listing first 45 summaries

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6: /cgn2_6/ptodata/1/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	87	9.8	248	US-09-621-976-9776	Sequence 9776, Ap
2	26	2.9	204	US-09-513-999C-27772	Sequence 27772, A
3	20	2.2	229	US-08-639-763-17	Sequence 17, Appl
4	20	2.2	229	US-08-639-763-18	Sequence 18, Appl
5	20	2.2	229	US-09-171-755B-17	Sequence 17, Appl
6	20	2.2	229	US-09-171-755B-18	Sequence 18, Appl
7	20	2.2	1740	US-09-023-655-1110	Sequence 1110, Ap
8	20	2.2	1907	US-08-184-327A-3	Sequence 3, Appl1
9	20	2.2	1907	PCT-US95-00670-3	Sequence 3, Appl1
10	20	2.2	2034	US-08-078-311-15	Sequence 15, Appl
11	20	2.2	2034	US-08-460-402-15	Sequence 15, Appl
12	19	2.1	448	US-09-621-976-8768	Sequence 8768, Ap
13	19	2.1	455	US-09-621-976-8742	Sequence 8742, Ap
14	19	2.1	465	US-09-621-976-8732	Sequence 8732, Ap
15	19	2.1	468	US-09-621-976-8667	Sequence 8667, Ap
16	19	2.1	476	US-09-621-976-8751	Sequence 8751, Ap
17	19	2.1	483	US-09-621-976-14600	Sequence 14600, A
18	19	2.1	770	US-09-976-594-997	Sequence 997, App
19	18	2.0	825	US-09-252-991A-4178	Sequence 4178, Ap
20	18	2.0	945	US-09-489-039A-4719	Sequence 4719, Ap
21	18	2.0	984	US-09-252-991A-4635	Sequence 4635, Ap
22	18	2.0	1171	US-08-336-257A-1	Sequence 1, Appl1
23	18	2.0	1171	5386025-1	Patent No. 5386025
24	18	2.0	1258	US-09-016-434-1294	Sequence 1294, Ap
25	18	2.0	1377	US-09-252-991A-4240	Sequence 4240, Ap
26	18	2.0	2094	US-09-252-991A-4535	Sequence 4535, Ap
27	18	2.0	71989	US-09-443-501A-2	Sequence 2, Appl1

C	28	18	2.0	1664976	4	US-08-916-421B-1	Sequence 1, Appl1
C	29	18	2.0	1664976	4	US-09-692-570-1	Sequence 1, Appl1
C	30	17	1.9	108	4	US-09-445-247-17	Sequence 17, Appl1
C	31	17	1.9	222	4	US-09-248-796A-10943	Sequence 10943, A
C	32	17	1.9	449	4	US-09-621-976-8678	Sequence 8678, Ap
C	33	17	1.9	570	4	US-09-016-434-789	Sequence 789, Appl
C	34	17	1.9	1050	1	US-08-180-209B-16	Sequence 16, Appl1
C	35	17	1.9	1050	1	US-08-385-745-16	Sequence 16, Appl1
C	36	17	1.9	1050	3	US-08-485-388-16	Sequence 16, Appl1
C	37	17	1.9	1050	3	US-08-474-853-16	Sequence 16, Appl1
C	38	17	1.9	1050	3	US-09-166-205B-16	Sequence 16, Appl1
C	39	17	1.9	1050	5	PCT-US94-02629-16	Sequence 16, Appl1
C	40	17	1.9	1221	1	US-08-229-287-3	Sequence 3, Appl1
C	41	17	1.9	1449	4	US-09-710-279-23	Sequence 23, Appl1
C	42	17	1.9	1509	4	US-09-724-797-89	Sequence 89, Appl1
C	43	17	1.9	1636	4	US-09-023-655-1005	Sequence 1005, Ap
C	44	17	1.9	1725	3	US-09-134-001C-2572	Sequence 2572, Ap
C	45	17	1.9	2007	3	US-09-052-089A-7	Sequence 7, Appl1

ALIGNMENTS

RESULT 1
US-09-621-976-9776/c
Sequence 9776, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
TITLE OF INVENTION: ESTs and Encoded Human Proteins.
FILE REFERENCE: GENSET 054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 9776
LENGTH: 248
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: 188
OTHER INFORMATION: n=a, g, c or t
US-09-621-976-9776
Query Match 9.8%; Score 87; DB 4; Length 248;
Best Local Similarity 100.0%; Pred. No. 1.1e-33;
Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 293 CTGAACCTGAGCTGTGCCCCCTGAACCGCTTGAACGAGATCTCTCAACCTTCCCGGC 352
Db 186 CTGAACCTGAGCTGTGCCCCCTGAACCGCTTGAACGAGATCTCTCAACCTTCCCGGC 127
Qy 353 CTGACGACCTTGCGCGGCGAGACCCC 379
Db 126 CTGACGACCTTGCGCGGCGAGACCCC 100
RESULT 2
US-09-513-999C-27772/c
Sequence 27772, Application US/09513999C
Patent No. 6783961
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Duclert, A.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
Patent No. 6783961
FILE REFERENCE: 59.US2.REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24

;; PRIOR APPLICATION NUMBER: US 60/122,487
;; PRIOR FILING DATE: 1999-02-26
;; NUMBER OF SEQ ID NOS: 36681
;; SOFTWARE: Patent.pm
;; SEQ ID NO 27772
;; LENGTH: 204
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-09-513-999C-27772

Query Match 2.9%; Score 26; DB 4; Length 204;
Best Local Similarity 100.0%; Pred. No. 0.0032;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 744 CTCGCCACCGGCTTCTTCGCGCGC 769
DB 26 CTCGCCACCGGCTTCTTCGCGCGC 1

RESULT 3
US-08-639-763-17
; Sequence 17, Application US/08639763
; Patent No. 5712127
; GENERAL INFORMATION:
; APPLICANT: Genescope, Inc.
; TITLE OF INVENTION: SUBSTRUCTIVE AMPLIFICATION
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David J. Wertz, Wilson Sonsini Goodrich & Rosati
; STREET: 650 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1050
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; OPERATING SYSTEM: IBM compatible
; SOFTWARE: Wordperfect for windows 6.1,
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/639,763
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/639,763
; FILING DATE: 29-APRIL-96
; ATTORNEY/AGENT INFORMATION:
; NAME: David J. Wertz
; REGISTRATION NUMBER: 38,362
; REFERENCE/DOCKET NUMBER: GENE 4001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 493-9300
; TELEFAX: (415) 493-6811
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 229 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-639-763-17

Query Match 2.2%; Score 20; DB 1; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 81 GCTCCTGGGGATCTGCTCC 100
DB 72 GCTCCTGGGGATCTGCTCC 91

RESULT 4
US-08-639-763-18/c

;; Sequence 18, Application US/08639763
;; Patent No. 5712127
;; GENERAL INFORMATION:
;; APPLICANT: Genescope, Inc.
;; TITLE OF INVENTION: SUBSTRUCTIVE AMPLIFICATION
;; NUMBER OF SEQUENCES: 27
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: David J. Wertz, Wilson Sonsini Goodrich & Rosati
;; STREET: 650 Page Mill Road
;; CITY: Palo Alto
;; STATE: California
;; COUNTRY: USA
;; ZIP: 94304-1050
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: 3.5 inch diskette
;; OPERATING SYSTEM: IBM compatible
;; SOFTWARE: Wordperfect for windows 6.1,
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/639,763
;; FILING DATE:
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/639,763
;; FILING DATE: 29-APRIL-96
;; ATTORNEY/AGENT INFORMATION:
;; NAME: David J. Wertz
;; REGISTRATION NUMBER: 38,362
;; REFERENCE/DOCKET NUMBER: GENE 4001
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 493-9300
;; TELEFAX: (415) 493-6811
;; INFORMATION FOR SEQ ID NO: 18:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 229 nucleotides
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
US-08-639-763-18

Query Match 2.2%; Score 20; DB 1; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 81 GCTCCTGGGGATCTGCTCC 100
DB 158 GCTCCTGGGGATCTGCTCC 139

RESULT 5
US-09-171-755B-17
; Sequence 17, Application US/09171755B
; Patent No. 6498024
; GENERAL INFORMATION:
; APPLICANT: MALEK, Lawrence T.
; APPLICANT: SOONANAN, Roy R.
; TITLE OF INVENTION: SUBSTRUCTIVE AMPLIFICATION KIT USEFUL IN THE DIAGNOSIS OF
; FILE REFERENCE: G01D 0181US
; CURRENT APPLICATION NUMBER: US/09/171,755B
; PRIOR FILING DATE: 1999-03-18
; PRIOR APPLICATION NUMBER: PCT/US97/07253
; PRIOR FILING DATE: 1997-04-29
; PRIOR APPLICATION NUMBER: US 08/639,763
; PRIOR FILING DATE: 1996-04-29
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 229
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-171-755B-17

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Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 72 GCTCTGGGGATCCTGTC 91

RESULT 6
US-09-171-755B-18/c
Sequence 18, Application US/09171755B
Patent No. 6498024
GENERAL INFORMATION:
APPLICANT: MALEK, Lawrence T.
APPLICANT: SOOKNANAN, Roy R.
TITLE OF INVENTION: SUBSTRUCTIVE AMPLIFICATION KIT USEFUL IN THE DIAGNOSIS OF
FILE REFERENCE: GOND-018US
CURRENT APPLICATION NUMBER: US/09/171.755B
PRIOR FILING DATE: 1999-03-18
PRIOR APPLICATION NUMBER: PCT/US97/07253
PRIOR FILING DATE: 1997-04-29
PRIOR APPLICATION NUMBER: US 08/639,763
PRIOR FILING DATE: 1996-04-29
NUMBER OF SEQ ID NOS: 38
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 18
LENGTH: 229
TYPE: DNA
ORGANISM: Homo sapiens
US-09-171-755B-18

Query Match 2.2%; Score 20; DB 4; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 81 GCTCTGGGGATCCTGTC 100
DB 158 GCTCTGGGGATCCTGTC 139

RESULT 7
US-09-023-655-1110
Sequence 1110, Application US/09023655
Patent No. 6607879
GENERAL INFORMATION:
APPLICANT: Cocks, Benjamin G.
APPLICANT: Susan G. Stuart
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023.655
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:

CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1110:
SEQUENCE CHARACTERISTICS:
LENGTH: 1740 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: g184262
US-09-023-655-1110

Query Match 2.2%; Score 20; DB 4; Length 1740;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 81 GCTCTGGGGATCCTGTC 100
DB 800 GCTCTGGGGATCCTGTC 819

RESULT 8
US-08-184-327A-3
Sequence 3, Application US/08184327A
Patent No. 5498599
GENERAL INFORMATION:
APPLICANT: Choi, Esther S.
APPLICANT: Hokom, Martha M.
APPLICANT: Hunt, Pamela
APPLICANT: Nichol, Janet L.
TITLE OF INVENTION: Compositions And Methods For Stimulating
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc., U.S. Patent Operations/RRC
STREET: 1840 DeHavilland Drive
CITY: Thousand Oaks
STATE: CA
COUNTRY: USA
ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/184,327A
FILING DATE: 20-JAN-1994
CLASSIFICATION: 514
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1907 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1905
US-08-184-327A-3

Query Match 2.2%; Score 20; DB 1; Length 1907;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 81 GCTCTGGGGATCCTGTC 100

Db 800 GCTCCTGGGATCCTGTCC 819

RESULT 9

PCT-US95-00670-3
Sequence 3, Application PC/TUS9500670
GENERAL INFORMATION:
APPLICANT: Choi, Esther S.
APPLICANT: Hokom, Martha M.
APPLICANT: Hunt, Pamela
APPLICANT: Nichol, Janet L.
TITLE OF INVENTION: Compositions And Methods For Stimulating
TITLE OF INVENTION: Platelet Production
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc., U.S. Patent Operations/RRC
STREET: 1840 DeHavilland Drive
CITY: Thousand Oaks
STATE: CA
COUNTRY: USA
ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/00670
FILING DATE: 18-JAN-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/184,327
FILING DATE: 20-JAN-1994
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1907 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1905
PCT-US95-00670-3

Query Match 2.2%; Score 20; DB 5; Length 1907;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 81 GCTCCTGGGATCCTGTCC 100
Db 800 GCTCCTGGGATCCTGTCC 819

RESULT 10

US-08-078-311-15
Sequence 15, Application US/08078311
Patent No. 5925750
GENERAL INFORMATION:
APPLICANT: Charon, Martine
APPLICANT: Gieselbrecht, Silvie
APPLICANT: Penciolelli, Jean-Francios
APPLICANT: Souyri, Michele
APPLICANT: Tambourin, Pierre
APPLICANT: Varlet, Paule
APPLICANT: Vigon, Isabelle
APPLICANT: Wendling, Francoise
TITLE OF INVENTION: Polypeptide of a Growth Factor Receptor
TITLE OF INVENTION: Family, Application in the Diagnosis and Treatment of
TITLE OF INVENTION: Myeloproliferative Disease
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:

ADDRESSEE: Merchant & Gould
STREET: 3100 No. 5925750west Center
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/078,311
FILING DATE: 18-JUN-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/FR90/00762
FILING DATE: 19-OCT-1990
ATTORNEY/AGENT INFORMATION:
NAME: Kowalczyk, Katherine M.
REGISTRATION NUMBER: 36,848
REFERENCE/DOCKET NUMBER: 8076.84USWO
TELEPHONE: 612-332-5300
TELEFAX: 612-332-9081
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 2034 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 4..1908
US-08-078-311-15

Query Match 2.2%; Score 20; DB 2; Length 2034;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 81 GCTCCTGGGATCCTGTCC 100
Db 803 GCTCCTGGGATCCTGTCC 822

RESULT 11

US-08-460-402-15
Sequence 15, Application US/08460402
Patent No. 5989833
GENERAL INFORMATION:
APPLICANT: Charon, Martine
APPLICANT: Gieselbrecht, Silvie
APPLICANT: Penciolelli, Jean-Francios
APPLICANT: Souyri, Michele
APPLICANT: Tambourin, Pierre
APPLICANT: Varlet, Paule
APPLICANT: Vigon, Isabelle
APPLICANT: Wendling, Francoise
TITLE OF INVENTION: Polypeptide of a Growth Factor Receptor
TITLE OF INVENTION: Family, Application in the Diagnosis and Treatment of
TITLE OF INVENTION: Myeloproliferative Disease
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
STREET: 90 South 7th Street, 3100 No. 5989833west Center
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,402
FILING DATE:
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/309,259
FILING DATE: 20-SEP-1994
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/078,311
FILING DATE: 18-JUN-1993
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: NO PCT/FR90/00762
FILING DATE: 14-OCT-1990
ATTORNEY/AGENT INFORMATION:
NAME: Randall A. Hillson
REGISTRATION NUMBER: 31,838
REFERENCE/DOCKET NUMBER: 8076.84US03
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-332-5300
TELEFAX: 612-332-9081
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 2034 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 4..1908
US-08-460-402-15

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Best Local Similarity 100.0%; Pred. No. 3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 803 GCTCTGGGATCTGCTCC 822
RESULT 12
US-09-621-976-8768/c
Sequence 8768, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTs and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 8768
LENGTH: 448
TYPE: DNA
ORGANISM: Homo sapiens
US-09-621-976-8768

Query Match 2.1%; Score 19; DB 4; Length 448;
Best Local Similarity 100.0%; Pred. No. 9.7;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 505 CATCTCCAGGACCCACGC 523
DB 387 CATCTCCAGGACCCACGC 369

RESULT 13
US-09-621-976-8742/c
Sequence 8742, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTs and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 8742
LENGTH: 455
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: 225
OTHER INFORMATION: n=a, g, c or t
US-09-621-976-8742

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Best Local Similarity 100.0%; Pred. No. 9.7;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 389 CATCTCCAGGACCCACGC 371

RESULT 14
US-09-621-976-8732/c
Sequence 8732, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTs and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 8732
LENGTH: 465
TYPE: DNA
ORGANISM: Homo sapiens
US-09-621-976-8732

Query Match 2.1%; Score 19; DB 4; Length 465;
Best Local Similarity 100.0%; Pred. No. 9.7;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 397 CATCTCCAGGACCCACGC 379

RESULT 15
US-09-621-976-8667/c
Sequence 8667, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTs and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2

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; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 8667
; LENGTH: 468
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-8667

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Query Match      2.1%; Score 19; DB 4; Length 468;
Best Local Similarity 100.0%; Pred.No. 9.7;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      394 CATTCAGGACCCACGAC 376

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Search completed: January 11, 2005, 11:40:27
 Job time : 114 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 11, 2005, 09:25:21 ; Search time 596 Seconds
(without alignments)
8577.830 Million cell updates/sec

Title: US-09-994-365-1
Perfect score: 891
Sequence: 1 ccccttgggggttcccgagca.....taaaatcatgttcttctaa 891

Scoring table: OLIGO_NIC
Gapop 60.0 , Gapept 60.0

Searched: 4293498 seqs, 2868903791 residues

Word size : 0

Total number of hits satisfying chosen parameters: 8586996

Minimum DB seq length: 0
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Post-processing: Listing first 45 summaries

Database :

Published Applications NA:*
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20: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
21: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	775	87.0	3001	9	US-09-994-365-4
4	724	81.3	25235	15	US-10-164-230-2
5	724	81.3	55050	17	US-10-467-752-4
6	554	62.2	565	15	US-10-029-386-5700
7	157	17.6	157	15	US-10-029-386-19510
8	60	6.7	60	10	US-09-908-975-5077
9	50	5.6	50	16	US-10-131-827-532
10	33	3.7	3673778	15	US-10-312-841-1
11	21	2.4	21	9	US-09-994-365-11
12	21	2.4	3673778	15	US-10-312-841-2

C 13	20	2.2	331	9	US-09-960-352-3940	Sequence 3940, Ap
C 14	20	2.2	395	9	US-09-960-352-5881	Sequence 5881, Ap
C 15	20	2.2	411	9	US-09-960-352-4663	Sequence 4663, Ap
C 16	20	2.2	531	10	US-09-918-995-25552	Sequence 25552, A
C 17	20	2.2	636	13	US-10-027-632-140159	Sequence 140159, A
C 18	20	2.2	636	13	US-10-027-632-140160	Sequence 140160, A
C 19	20	2.2	636	15	US-10-027-632-140159	Sequence 140159, A
C 20	20	2.2	636	15	US-10-027-632-140160	Sequence 140160, A
C 21	20	2.2	692	9	US-09-764-864-429	Sequence 429, App
C 22	20	2.2	993	17	US-10-437-963-25592	Sequence 25592, A
C 23	20	2.2	1740	16	US-10-641-643-1110	Sequence 1110, Ap
C 24	20	2.2	2167	15	US-10-094-749-145	Sequence 145, App
C 25	20	2.2	202814	18	US-10-719-993-6812	Sequence 6812, App
C 26	20	2.2	1601042	13	US-10-027-632-59064	Sequence 59064, A
C 27	20	2.2	1601042	15	US-10-027-632-59064	Sequence 59064, A
C 28	19	2.1	19	9	US-09-994-365-12	Sequence 12, Appl
C 29	19	2.1	385	10	US-09-803-719-2243	Sequence 2243, Ap
C 30	19	2.1	458	9	US-09-864-761-10055	Sequence 10055, A
C 31	19	2.1	876	16	US-10-424-599-74654	Sequence 74654, A
C 32	19	2.1	1059	13	US-10-027-633-119721	Sequence 119721, A
C 33	19	2.1	1059	13	US-10-027-633-119722	Sequence 119722, A
C 34	19	2.1	1059	13	US-10-027-633-119723	Sequence 119723, A
C 35	19	2.1	1059	15	US-10-027-633-119721	Sequence 119721, A
C 36	19	2.1	1059	15	US-10-027-633-119722	Sequence 119722, A
C 37	19	2.1	1059	15	US-10-027-633-119723	Sequence 119723, A
C 38	19	2.1	15853	16	US-10-221-613-422	Sequence 422, App
C 39	19	2.1	59588	15	US-10-017-161-2233	Sequence 2233, Ap
C 40	19	2.1	73145	13	US-10-087-192-274	Sequence 1879, Ap
C 41	19	2.1	87394	18	US-10-810-788A-6	Sequence 274, App
C 42	19	2.1	110079	14	US-10-175-523-96	Sequence 6, Appl
C 43	19	2.1	197526	17	US-10-322-281-498	Sequence 96, Appl
C 44	19	2.0	18	15	US-10-164-230-23	Sequence 498, App
C 45	18	2.0	18	15	US-10-164-230-23	Sequence 23, Appl

ALIGNMENTS

RESULT 1
US-09-994-365-1
; Sequence 1, Application US/0994365
; Patent No. US20020115148A1
; GENERAL INFORMATION:
; APPLICANT: Charmsley, Patrick
; APPLICANT: Mose, Patrick
; APPLICANT: McEuen, Mark
; TITLE OF INVENTION: Compositions and Methods for Diagnosing or Treating Psoriasis
; FILE REFERENCE: CECH118109
; CURRENT APPLICATION NUMBER: US/09/994,365
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: US 60/253,592
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 60/256,839
; PRIOR FILING DATE: 2000-12-15
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 891
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (64)..(471)
US-09-994-365-1

Query Match 100.0%; Score 891; DB 9; Length 891;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 891; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTCTTGGGGTTCCCGAGCAGCAGTCAAGCCACCCAGCTTTGGGGGCGGTACATA 60
DB 1 CCTCTTGGGGTTCCCGAGCAGCAGTCAAGCCACCCAGCTTTGGGGGCGGTACATA 60

QY 61 GCCATGATCTCTCAATGGAAGCTCTGGGATCTGTGCTTTGCTGCAACAGAGGC 120
 Db 61 GCCATGATCTCTCAATGGAAGCTCTGGGATCTGTGCTTTGCTGCAACAGAGGC 120
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 Db 121 ATCTCAGGACGAGGAGGACACCTCTCTCAACCCAGGAGACCGAGAGAGGAGGC 180
 QY 181 TCCCAACATGCTCTCAGAGGCCCCCAGTCCCGGTGACCTTGGCCAGAGGAGCCCCCT 240
 Db 181 TCCCAACATGCTCTCAGAGGCCCCCAGTCCCGGTGACCTTGGCCAGAGGAGCCCCCT 240
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 QY 361 CTTTGGCCGAGAGACCCAGACCCCGAGAGAACCCCTGCTGCTGCTGAGAGTGAAC 420
 Db 361 CTTTGGCCGAGAGACCCAGACCCCGAGAGAACCCCTGCTGCTGCTGAGAGTGAAC 420
 QY 421 AACGACCTCAGAGAGACGACCTTGAACCCAGGAGAGAGTACAGATTAATGAGT 480
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 QY 481 CCCCCTGAGCGTCTGTCCAGGACATCTCCAGGACCCAGGCGCTTCAACCTCTGAT 540
 Db 481 CCCCCTGAGCGTCTGTCCAGGACATCTCCAGGACCCAGGCGCTTCAACCTCTGAT 540
 QY 541 TCCCGTGAATCTTCCCAATTTAGCCTATCTCTTAACTCTTCTCAATCCCTGAT 600
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 QY 601 TTTATTTGAAACCGGTAAAGTGTGTCTCAATTTCTGCTGCTCTCTGAGATCA 660
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 QY 721 CTCAGGCTCTCGGCCCCACCTACCTCCACCCGCTCTTCTGCGCGGAGTCTGAGG 780
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 QY 781 CAGGCTATGTAATGTGTCTTCTCTGCACTGTGTGCGGCGGAGAGTATCAT 840
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 Db 841 AGACAGCTGCTCTCCATGAAACGAAAAATTAATCATGTTTCTTAA 891

RESULT 2
 ; Sequence 10, Application US/09994365
 ; Patent No. US20020115148A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Charmsley, Patrick
 ; APPLICANT: Moss, Patrick
 ; APPLICANT: McEuen, Mark
 ; TITLE OF INVENTION: Compositions and Methods for Diagnosing or Treating Peorlasia
 ; FILE REFERENCE: CECH118109
 ; CURRENT APPLICATION NUMBER: US/09/994,365
 ; PRIOR FILING DATE: 2001-11-26
 ; PRIOR APPLICATION NUMBER: US 60/253,592
 ; PRIOR FILING DATE: 2000-11-28
 ; PRIOR APPLICATION NUMBER: US 60/256,839
 ; PRIOR FILING DATE: 2000-12-15

; NUMBER OF SEQ ID NOS: 16
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 10
 ; LENGTH: 2997
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-994-365-10

Query Match 87.0%; Score 775; DB 9; Length 2997;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 775; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 QY 237 CCGCTCTTTGAAGATCTCTCCGCTTACCCGCCCCAGTCTCTCTGAGAGAGGAGG 296
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 QY 2320 CCGCTCTTTGAAGATCTCTCCGCTTACCCGCCCCAGTCTCTCTGAGAGAGGAG 2379
 Db 2320 CCGCTCTTTGAAGATCTCTCCGCTTACCCGCCCCAGTCTCTCTGAGAGAGGAG 2379
 QY 297 AACTGAGTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 356
 Db 297 AACTGAGTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 356
 QY 357 CAGACCTTTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 416
 Db 357 CAGACCTTTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 416
 QY 2440 CAGACCTTTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2499
 Db 2440 CAGACCTTTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2499
 QY 417 GGAACAACGAGCTCAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 476
 Db 417 GGAACAACGAGCTCAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 476
 QY 2500 GGAACAACGAGCTCAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2559
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 QY 657 CATACTTACTCTCAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 716
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 QY 717 TGGCCCTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 776
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 QY 2800 TGGCCCTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2859
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 QY 777 GGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 836
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RESULT 3
 ; Sequence 4, Application US/09994365
 ; Patent No. US20020115148A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Charmsley, Patrick
 ; APPLICANT: Moss, Patrick
 ; APPLICANT: McEuen, Mark

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OY	597	CGGTTTATTTCTGAACCCGTAAGGAGTGTCTCAATATTTCTGTCGCCCTCCGAGATC	656
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OY	657	CATACTTAGTCTTCACATCGCCCGTTTCTCTGACAGCCTAAGCCTACTCTCTAAC	716
Db	2293	CATACTTAGTCTTCACATCGCCCGTTTCTCTGACAGCCTAAGCCTACTCTCTAAC	2352
OY	717	TGCGCTCAGGCGCTCGGCCCAACCTCCACCCCGGCTTCTCTGCGCGGCGCATGCT	776
Db	2353	TGCGCTCAGGCGCTCGGCCCAACCTCCACCCCGGCTTCTCTGCGCGGCGCATGCT	2412
OY	777	GGGGCAGGGCTATGCTACTGTGTTCCTTCTGCACTGTGCGCGCGGCGGAGAACTAT	836
Db	2413	GGGGCAGGGCTATGCTACTGTGTTCCTTCTGCACTGTGCGCGCGGCGGAGAACTAT	2472
OY	837	CAGTAGACAGCGCTGCTTCCATGAAAGGAAAAATTAATTCATGTTTCTTAA	891
Db	2473	CAGTAGACAGCTGCTTCCATGAAAGGAAAAATTAATTCATGTTTCTTAA	2527

RESULT 5
US-10-467-752-4

APPLICANT: Lench, et al.
TITLE OF INVENTION: Test and Model for Inflammatory diseases

CURRENT APPLICATION NUMBER: US/10/467,752

PRIOR APPLICATION NUMBER: PCT/GB02/006533

PRIOR APPLICATION NUMBER: GB0103514.6

NUMBER OF SEQ ID NOS: 109

; SEQ ID NO 4

TYPE: DNA

FEATURE:

LOCATION: (13351) .. (13351)

FEATURE:

LOCATION: (13401) .. (13401)

US-10-467-752-4

Query Match	81.3%;	Score 724;	DB 17;	Length 55050;
-------------	--------	------------	--------	---------------

Matches 774; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

117 AGGCATCTCAGGCAGCGGGCCACCCCTCTCACCACCCGAGAGGACCGAGAGGCGC 176

Db	27098	AGGATCTCAGGACGACGAGGGCCACCCCTCTCACCCACCCGACAGAGACCCGAAAGAGAGGC	27157
QY	177	AGGCTCCCAACATTGCTCTAGAGGCCCCCAAGTCCCGGTGATCCTTTGACCTTTGGCCAGAGGACC	236
Db	27158	AGGCTCCCAACATTGCTCTAGAGGCCCCCAAGTCCCGGTGACCTTTGGCCAGAGGAGCC	27217
QY	237	CCCTCTCTTGAAGAATCTCTCCGCTTACCGGCCCCAGTCTGCTTGTGAAGACCTTGCTGA	296
Db	27218	CCCTCTCTTGAAGAATCTCTCCGCTTACCGGCCCCAGTCTGCTTGTGAAGACCTTGCTGA	27277
QY	297	AACTGAAGTCTGGCCCCCTGAAACGACCTTAAGACGATCTCTCAACCTCCCGGACTGA	356
Db	27278	AACTGAAGTCTGGCCCCCTGAAACGACCTTAAGACGATCTCTCAACCTCCCGGACTGA	27337
QY	357	CGACCTTTGGCCGACAGACCCCAAGCCCAAGAAAACCCCTGGCTCTTGCCCTGAGGT	416
Db	27338	CGACCTTTGGCCGACAGACCCCAAGCCCAAGAAAACCCCTGGCTCTTGCCCTGAGGT	27397
QY	417	GGACAAACCGACTCTAGAGAGAGCCAGACTTAAGCCACCCCGGAAAGATGACGATTAAG	476
Db	27398	GGACAAACCGACTCTAGAGAGAGCCAGACTTAAGCCACCCCGGAAAGATGACGATTAAG	27457
QY	477	GAGTCCGCTGAGCGGTTCTGTTCCAGGACATCTCAAGGACCGACGCGCTCTCAACCTC	536
Db	27458	GAGTCCGCTGAGCGGTTCTGTTCCAGGACATCTCAAGGACCGACGCGCTCTCAACCTC	27517
QY	537	TGATTTCCCGGTGAATCTTCCCAATTAGACTTCTCTTAAACCTTTCTCATTCCTT	596
Db	27518	TGATTTCCCGGTGAATCTTCCCAATTAGACTTCTCTTAAACCTTTCTCATTCCTT	27577
QY	597	CGGTTTATTTCTGAACCCGTAAGGTGTGTTCTCAATATTCTCTGTCCTCTGTGATTC	656
Db	27578	CGGTTTATTTCTGAACCCGTAAGGTGTGTTCTCAATATTCTCTGTCCTCTGTGATTC	27637
QY	657	CATACCTTAGTCCACAAATGCGCGGTTTTTCCCTGACAGCCTAAGACTACTCTCTAC	716
Db	27638	CATACCTTAGTCCACAAATGCGCGGTTTTTCCCTGACAGCCTAAGACTACTCTCTAC	27697
QY	717	TGCGCTTCAGAGCCTCGGCCCCCACTACCTCCACCGGATCTTCTGCGCGGAGTGGCT	776
Db	27698	TGCGCTTCAGAGCCTCGGCCCCCACTACCTCCACCGGATCTTCTGCGCGGAGTGGCT	27757
QY	777	GGGGCAGGCTATAGTATCTGTGTTCCCTTCTGCACTGGTGGCGGGCGGCAAGAACTAT	836
Db	27758	GGGGCAGGCTATAGTATCTGTGTTCCCTTCTGCACTGGTGGCGGGCGGCAAGACTAT	27817
QY	837	CAGTAGACACACTGCTGCTTCATGAAGCGAAAAAATTAATATCATCTTTCTTAA	891
Db	27818	CAGTAGACACACTGCTGCTTCATGAAGCGAAAAAATTAATATCATCTTTCTTAA	27872

RESULT 6

; Sequence 5700, Application US/10029386

GENERAL INFORMATION:

APPLICANT: Rank, David R.

TITLE OF INVENTION: HUMAN GENOME-DERIVED SIN...

FILE REFERENCE: AEOMICA-X-2
CUMMINS ADDITION NUMBER: 70/10/000 100

CURRENT FILING DATE: 2001-12-20

```

; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; CEO ID NO. 5700

```

LENGTH: 565
TYPE: DATA

ORGANISM: *Homo sapiens*

OTHER INFORMATION: MAP TO AB023060.1


```

RESULT 9
US-10-131-827-532
: Sequence 532, Application US/10131827
: Publication No. US20040009479A1
: GENERAL INFORMATION:
: APPLICANT: Womigemuth, Jay
: APPLICANT: Fry, Kirk
: APPLICANT: Woodward, Robert
: APPLICANT: Ly, Ngoc
: TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
: TITLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES
: FILE REFERENCE: 506612000120

```

CURRENT APPLICATION NUMBER: US/10/131,827
CURRENT FILING DATE: 2002-09-06
PRIOR APPLICATION NUMBER: US 10/006,290
PRIOR FILING DATE: 2001-10-22
PRIOR APPLICATION NUMBER: US 60/296,764
PRIOR FILING DATE: 2001-06-08
NUMBER OF SEQ ID NOS: 9090
SOFTWARE: PatentIn version 3.1
SEQ ID NO 532
LENGTH: 50
TYPE: DNA
ORGANISM: Homo sapiens
US-10-131-827-532

Query Match 5.6%; Score 50; DB 16; Length 50;
Best Local Similarity 100.0%; Pred. No. 2.5e-15;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 820 CCGCGCGAGAGACTATGAGACAGCTGCTTCATGAAACGAAA 869
DB 1 CCGCGCGAGAGACTATGAGACAGCTGCTTCATGAAACGAAA 50

RESULT 10
US-10-312-841-1/c
Sequence 1, Application US/10312841
Publication No. US20030186277A1
GENERAL INFORMATION:
APPLICANT: Epigenomics AG
TITLE OF INVENTION: Diagnose von bedeutenden genetischen Parametern innerhalb des MHC
FILE REFERENCE: E01/1208/WO
CURRENT APPLICATION NUMBER: US/10/312,841
CURRENT FILING DATE: 2002-12-30
NUMBER OF SEQ ID NOS: 2
SEQ ID NO 1
LENGTH: 3673778
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens).
FEATURE:
NAME/KEY: unsure
LOCATION: (3294164)
US-10-312-841-1

Query Match 3.7%; Score 33; DB 15; Length 3673778;
Best Local Similarity 100.0%; Pred. No. 6.4e-07;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 566 CCTATCTCCTTAACCTCTTCATTCCTCG 598
DB 1425602 CCTATCTCCTTAACCTCTTCATTCCTCG 1425570

RESULT 11
US-09-994-365-11
Sequence 11, Application US/09994365
Patent No. US20020115148A1
GENERAL INFORMATION:
APPLICANT: Charmley, Patrick
APPLICANT: Moss, Patrick
APPLICANT: McEuen, Mark
TITLE OF INVENTION: Compositions and Methods for Diagnosing or Treating Psoriasis
FILE REFERENCE: CECH18109
CURRENT APPLICATION NUMBER: US/09/994,365
CURRENT FILING DATE: 2001-11-26
PRIOR APPLICATION NUMBER: US 60/253,592
PRIOR FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: US 60/256,839
PRIOR FILING DATE: 2000-12-15
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn version 3.0
SEQ ID NO 11

LENGTH: 21
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(21)
OTHER INFORMATION: PCR Primer DMO 9299
US-09-994-365-11

Query Match 2.4%; Score 21; DB 9; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 GACTCAGCCCAACCCAGCTTT 45
DB 1 GACTCAGCCCAACCCAGCTTT 21

RESULT 12
US-10-312-841-2
Sequence 2, Application US/10312841
Publication No. US20030186277A1
GENERAL INFORMATION:
APPLICANT: Epigenomics AG
TITLE OF INVENTION: Diagnose von bedeutenden genetischen Parametern innerhalb des MHC
FILE REFERENCE: E01/1208/WO
CURRENT APPLICATION NUMBER: US/10/312,841
CURRENT FILING DATE: 2002-12-30
NUMBER OF SEQ ID NOS: 2
SEQ ID NO 2
LENGTH: 3673778
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
FEATURE:
NAME/KEY: unsure
LOCATION: (379615)
US-10-312-841-2

Query Match 2.4%; Score 21; DB 15; Length 3673778;
Best Local Similarity 100.0%; Pred. No. 1.2; Mismatches 0; Indels 0; Gaps 0;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 858 ATGAAACGAGAAATATAAT 878
DB 2248469 ATGAAACGAGAAATATAAT 2248489

RESULT 13
US-09-960-352-3940/c
Sequence 3940, Application US/09960352
Patent No. US20020137139A1
GENERAL INFORMATION:
APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 3940
LENGTH: 331
TYPE: DNA
ORGANISM: Bos taurus
OTHER INFORMATION: Clone ID: 17-LIB34-027-Q1-E1-E9
US-09-960-352-3940

Query Match 2.2%; Score 20; DB 9; Length 331;
Best Local Similarity 100.0%; Pred. No. 10;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 195 TCAGGGCCCCCAGTCCCG 214
 |||||
 Db 63 TCAGGGCCCCCAGTCCCG 44

RESULT 14
 US-09-960-352-5881/C
 ; Sequence 5881, Application US/09960352
 ; Patent No. US20020137139A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Warren, Wesley C.
 ; APPLICANT: Tao, Nengbing
 ; APPLICANT: Byatt, John C.
 ; APPLICANT: Mathalagan, Nagappan
 ; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
 ; FILE REFERENCE: 16511.006/37-21(10298)C
 ; CURRENT APPLICATION NUMBER: US/09/960,352
 ; CURRENT FILING DATE: 2001-09-24
 ; NUMBER OF SEQ ID NOS: 15112
 ; SEQ ID NO 5881
 ; LENGTH: 395
 ; TYPE: DNA
 ; ORGANISM: Bos taurus
 ; OTHER INFORMATION: Clone ID: 25-LIB34-044-Q1-E1-G1
 US-09-960-352-5881

Query Match 2.2%; Score 20; DB 9; Length 395;
 Best Local Similarity 100.0%; Pred. No. 9.8;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 195 TCAGGGCCCCCAGTCCCG 214
 |||||
 Db 72 TCAGGGCCCCCAGTCCCG 53

RESULT 15
 US-09-960-352-4663/C
 ; Sequence 4663, Application US/09960352
 ; Patent No. US20020137139A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Warren, Wesley C.
 ; APPLICANT: Byatt, John C.
 ; APPLICANT: Mathalagan, Nagappan
 ; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
 ; FILE REFERENCE: 16511.006/37-21(10298)C
 ; CURRENT APPLICATION NUMBER: US/09/960,352
 ; CURRENT FILING DATE: 2001-09-24
 ; NUMBER OF SEQ ID NOS: 15112
 ; SEQ ID NO 4663
 ; LENGTH: 411
 ; TYPE: DNA
 ; ORGANISM: Bos taurus
 ; OTHER INFORMATION: Clone ID: 20-LIB34-020-Q1-E2-E7
 US-09-960-352-4663

Query Match 2.2%; Score 20; DB 9; Length 411;
 Best Local Similarity 100.0%; Pred. No. 9.8;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 195 TCAGGGCCCCCAGTCCCG 214
 |||||
 Db 349 TCAGGGCCCCCAGTCCCG 330

Search completed: January 11, 2005, 11:50:40
 Job time : 609 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: January 11, 2005, 09:34:16 ; Search time 431.936 Seconds
(without alignments)
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Title: US-09-994-365-2
Perfect score: 808
Sequence: 1 MINMKLLGIVLCIHTRG.....EVDNRPOEPPDLPPEEYR 136

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Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

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Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

- 1: GeneSeq_23Sep04:*
- 2: GeneSeq1980s:*
- 3: GeneSeq1990s:*
- 4: GeneSeq2000s:*
- 5: GeneSeq2001as:*
- 6: GeneSeq2002as:*
- 7: GeneSeq2002bs:*
- 8: GeneSeq2003as:*
- 9: GeneSeq2003bs:*
- 10: GeneSeq2003cs:*
- 11: GeneSeq2003ds:*
- 12: GeneSeq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	808	100.0	891	ABK86962 Human can
2	808	100.0	1473	ABN60006 Novel hum
3	712	88.1	2997	ABK86967 Human CAN
4	712	88.1	3001	ABK86963 Human CAN
5	712	88.1	25235	AAH45310 Human SEE
6	712	88.1	55050	ABQ75680 Human SEE

7	486	60.1	565	12	ACH72505	Ach72505 Human gen
8	314	38.9	157	12	ACH86315	Ach86315 Human gen
9	199	24.6	711	8	ACA33990	ACA33990 Prokaryot
10	198.5	24.6	2772	8	ACA0420	ACA0420 Prokaryot
11	198.5	24.6	110000	4	AA199682_10	Continuation (11) o
12	198.5	24.6	110000	4	AA199683_10	Continuation (11) o
13	195.5	24.2	446	4	AA123276	Probe #13
14	195.5	24.2	446	4	ABA68382	Human foe
15	195.5	24.2	446	4	AA18596	Probe #17
16	195.5	24.2	446	4	ABA50433	Human bre
17	195.5	24.2	446	4	ABA35379	Probe #13
18	195.5	24.2	446	4	AAK42529	Human bon
19	195.5	24.2	446	4	AAK16757	Human bra
20	195.5	24.2	446	4	ABS42140	Human liv
21	195.5	24.2	446	5	AA108921	Probe #89
22	195.5	24.2	446	6	ABS16574	Human gen
23	195	24.1	12733	6	ABK98631	Vector pr
24	195	24.1	12733	6	ACD13882	L. lactis
25	195	24.1	12739	6	ABK98592	Vector pr
26	195	24.1	12739	9	ACD13843	Plasmid p
27	190.5	23.6	6313	2	AAQ29965	Sugar bee
28	189.5	23.5	110000	4	AA199682_09	Continuation (10) o
29	189.5	23.5	110000	4	AA199683_09	Continuation (10) o
30	188.5	23.3	600	6	ABQ52497	Abq52497 Oligonuc
31	188.5	23.3	600	6	ABQ52496	Abq52496 Oligonuc
32	188.5	23.3	110000	4	AA199682_27	Continuation (28) o
33	188.5	23.3	110000	4	AA199683_28	Continuation (28) o
34	188.5	23.3	110000	4	AA199683_27	Continuation (28) o
35	188	23.3	1493	12	ACH91938	Human gen
36	187.5	23.2	1327	6	ABQ68452	Abq68452 Listeria
37	187.5	23.2	3946	2	AA173610	At193610 Mycobacte
38	187	23.1	1833	4	AB122159	AB122159 Drosophi
39	186	23.0	1452	8	ACF39367	AcF39367 Mycobacte
40	186	23.0	1455	8	ACA40813	ACA40813 Prokaryot
41	186	23.0	110000	4	AA199682_37	Continuation (38) o
42	186	23.0	110000	4	AA199683_37	Continuation (38) o
43	185	22.9	110000	4	AA199682_40	Continuation (41) o
44	185	22.9	110000	4	AA199683_40	Continuation (41) o
45	184.5	22.8	110000	4	AA199683_11	Continuation (12) o

ALIGNMENTS

RESULT 1	
ABK86962	standard; cDNA; 891 BP.
AC	ABK86962;
DT	24-SEP-2002 (first entry)
DE	Human candidate coding sequence-1 (CAN-1) cDNA.
XX	Human; anti-psoriatic; chromosome 6; candidate coding sequence-1; CAN-1;
KW	SEER-1; STG; human leukocyte antigen C; HLA C; HLA Cw6; psoriasis; skin;
KW	keratinocyte; chronic inflammatory dermatosis; erythroderma; seborethic;
KW	gutrate; puerperal variant; Reiter's disease; hyperproliferation;
KW	epidermis; differentiation; diagnosis; gene therapy; gene; ss; SNP;
KW	single nucleotide polymorphism.
XX	Homo sapiens.
XX	
FT	Key
FT	CDS
FT	Location/Qualifiers
FT	64..474
FT	/*tag= a
FT	/product= "CAN-1"
FT	64..129
FT	sig_peptide
FT	/*tag= b
FT	130..471
FT	mat_peptide
FT	/*tag= c
FT	/note= "Mature CAN-1"
FT	variation
FT	/*tag= d

PT /standard_name= "Single nucleotide polymorphism"
XX
XX
PN MO200244375-A2.
XX
XX
PD 06-JUN-2002.
XX
XX
PF 27-NOV-2001; 2001MO-US044506.
XX
XX PR 28-NOV-2000; 2000US-0253592P.
PR 15-DEC-2000; 2000US-0256839P.
XX
XX
PA (CELL-) CELUTECH R & D INC.
XX
XX
PI Charmley P, `Moss P, Mceuen M;
XX
XX WPI; 2002-508513/54.
DR P-PSDB; AAU79579.
XX
XX
XX Novel isolated CAN-1 polypeptide involved in keratinocyte proliferation
PT and differentiation, and polynucleotides encoding the polypeptide; useful
PT for diagnosing or predicting susceptibility to psoriasis in individual.
XX
XX
XX Claim 8; Page 80-81; 95pp; English.

CC The invention discloses isolated candidate coding sequence-1 (CAN-1),
CC SEERK-1 (not defined) and STG (not defined) polypeptides, and the
CC polynucleotides encoding them. All three genes were identified due to
CC their proximity to the human leukocyte antigen C (HLA C) locus on
CC chromosome 6. The HLA Cw6 allele is associated with psoriasis and as the
CC three genes are expressed in normal skin and/or keratinocyte tissue, they
CC may also have a role in psoriasis. Psoriasis is a chronic inflammatory
CC dermatosis that is characterized by hyperproliferation of epidermal
CC cells. Possible treatments against psoriasis involve the inhibition of
CC movement of cells into the epidermis, or the inhibition of
CC hyperproliferation or abnormal differentiation of keratinocytes, by the
CC inhibition of the CAN-1, STG or SEERK-1 polypeptides binding to their
CC binding partners. The polypeptides are useful for diagnosing or
CC predicting the susceptibility to psoriasis in an individual, for
CC ameliorating the symptoms and/or progression of psoriasis and for
CC identifying agents useful for treating psoriasis or modulating the
CC activity of the polypeptide. The polypeptides are also useful for
CC enhancing the level of CAN-1, STG or SEERK-1 biological activity in a cell
CC or tissue. The nucleic acid molecules are useful as hybridisation probes
CC in diagnostic procedures (such as diagnosing the presence of psoriasis or
CC the propensity to develop psoriasis) and for suppressing the expression
CC of CAN-1 or STG gene (e.g. antisense inhibition, gene therapy).
CC Antibodies, raised against the polypeptides, are useful for decreasing
CC the level of CAN-1, STG or SEERK-1 biological activity in a cell. The
CC sequence presented is the human candidate coding sequence-1 (CAN-1) cDNA
XX

Sequence 891 BP; 169 A; 339 C; 196 G; 187 T; 0 U; 0 Other;

Alignment Scores:	
Pred. No.:	6.84e-29
Score:	808.00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	100.00%
DB:	6
US-09-994-365-2 (1-136) x ABR86962 (1-891)	
	Length: 891
	Matches: 136
	Conservative: 0
	Mismatches: 0
	Indels: 0
	Gaps: 0

Qy	Me11eleuAaStrpYpYsLeuIuengUy11eleuValIeuCyeLeuH1sThrArgUy1le	20
Db	ATATCTCTCACTGAGAGCTCTCGGGGATCTCGGTCTTTGGCTTCACACCAAGGGATCT	122
Qy	21 SerG1YserG1uag1Yh1sProSerH1sProProA1ag1uAspArg1uG1uAglYser	40
Db	124 TCAGGACGAGGGCCACCCCTTCTACCCACCGGAGAGACCGAGAGAGGCGAGCTCC	183
Qy	41 ProThrLeuProG1uYpProProVAlProG1YAspProTTrpProG1YAlAProProLeu	60
Db	184 CCACACTTGCTAGGGCCCCCAGTCCCGGTGACCTTGGCAGGGGACCCCCCTTCTC	243

OY	61	PheIuAspProProthraArgProSerArgProTyrAspLeuProGluIleThyGly	80
Db	244	TTTGAAAGATCTTCGGCTACCGCGCCCGTGTCTCTCGAGAGACTGCTGAAACTGGA	303
OY	81	ValIrrProBProGluProProArgThraspProGlnProProArgProAspAspPro	100
Db	304	GTCTGGCCCCCTGAACCGGCTGAAGAGATCTCTCAACTCCCGGCGTGAAGACCT	363
OY	101	TyrProAlaGlyProGlnProProGluAsnProTyrProProAlaProGluValAspAsn	120
Db	364	TGGCGGCGAGAACCCAGCGCCCGCAGAAAACTCTGTGCTCTCGCCCTGAGGTGACAAC	423
OY	121	ArgProGlnGluGluProAspLeuAspProProArgGluGluTyrArg	136
Db	424	CGACTTCAGAGAGCCAGACTTAAGCCACCCCGGGAAGTACAG	471

RESULT 2	
ID	ABN60006
XX	ABN60006 standard; cDNA; 1473 BP.
XX	AC
XX	ABN60006;
DT	28-JUN-2002 (first entry)
DE	Novel human coding sequence SEQ ID NO: 417.

KW Human; antiinfective; vulnereary; antiinflammatory; immunomodulator;
KW antiinfectility; cerebroprotective; cytoskeletal; rheumatic; gene therapy;
KW neuroprotective; antiparkinsonian; protein therapy; ESt,
KW expressed sequence tag; gene; ss.
XX
XX Homo sapiens.
OS

XX WO200222660-A2.
 XX
 EN
 XX
 PD
 21-MAR-2002.
 XX
 XX
 FF 10-SEP-2001, 2001WO-US026015.
 FF
 XX 11-SEP-2000, 2000US-00659671.
 PR

XX
PA (HYSE-) HYSEQ INC.
XX
XX Tang YT, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA, Ren F;
PI Xue AD, Yang Y, Wehrman T, Dimanac RT;
XX
XX WPI; 2002-292408/33.
DR P-PSDB; ABB97593.

PT An isolated polynucleotide for treating diseases associated with its
 PT encoded polypeptide such as cancer and multiple sclerosis.
 XX
 PS Claim 1, SEQ ID NO 417, 509pp, English.
 PS

The present invention provides the protein and coding sequences of novel human proteins. These were isolated from expressed sequences tags (ESTs). They can be used to stimulate cell growth, to regulate hematopoiesis e.g. to treat aplastic anaemia, to help tissue regrowth e.g. in burn treatment, to regulate the immune system e.g. to treat multiple sclerosis, to regulate activin or inhibin e.g. to treat infertility, to regulate haemostasis or thrombolysis e.g. to treat cancer, to screen for drugs, to treat inflammatory conditions e.g. rheumatoid arthritis, and to treat nervous system disorders e.g. Parkinson's disease. The present sequence is a coding sequence of the invention

Alignment Scores:		
Pred. No.:	1,01e-28	Length:
Score:	808.00	Matches:
Percent Similarity:	100.00%	Conservative:
		0

PI Charnley P, Moss P, Mceuen M;
 XX WPI; 2002-508513/54.
 DR P-PSDB; AAU79579.
 XX
 PT Novel isolated CAN-1 polypeptide involved in keratinocyte proliferation
 PT and differentiation, and polynucleotides encoding the polypeptide, useful
 PT for diagnosing or predicting susceptibility to psoriasis in individual.
 XX
 PS Claim 18; Page 82-84; 95pp; English.
 XX
 CC The invention discloses isolated candidate coding sequence-1 (CAN-1),
 CC SEEK-1 (not defined) and STG (not defined) polypeptides, and the
 CC polynucleotides encoding them. All three genes were identified due to
 CC their proximity to the human leukocyte antigen C (HLA C) locus on
 CC chromosome 6. The HLA Cw6 allele is associated with psoriasis and as the
 CC three genes are expressed in normal skin and/or keratinocyte tissue, they
 CC may also have a role in psoriasis. Psoriasis is a chronic inflammatory
 CC dermatosis that is characterised by hyperproliferation of epidermal
 CC cells. Possible treatments against psoriasis involve the inhibition of
 CC movement of cells into the epidermis, or the inhibition of
 CC hyperproliferation or abnormal differentiation of keratinocytes, by the
 CC inhibition of the CAN-1, STG or SEEK-1 polypeptides binding to their
 CC binding partners. The polypeptides are useful for diagnosing or
 CC predicting the susceptibility to psoriasis in an individual, for
 CC ameliorating the symptoms and/or progression of psoriasis and for
 CC identifying agents useful for treating psoriasis or modulating the
 CC activity of the polypeptide. The polypeptides are also useful for
 CC enhancing the level of CAN-1, STG or SEEK-1 biological activity in a cell
 CC or tissue. The nucleic acid molecules are useful as hybridisation probes
 CC in diagnostic procedures (such as diagnosing the presence of psoriasis or
 CC the propensity to develop psoriasis) and for suppressing the expression
 CC of CAN-1 or STG gene (e.g. antisense inhibition, gene therapy).
 CC Antibodies, raised against the polypeptides, are useful for decreasing
 CC the level of CAN-1, STG or SEEK-1 biological activity in a cell. The
 CC sequence presented is the human candidate coding sequence-1 (CAN-1)
 CC genomic DNA
 XX
 SQ Sequence 3001 BP; 619 A; 786 C; 914 G; 682 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 4.05e-24 Length: 3001
 Score: 712.00 Matches: 118
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 88.12% Indels: 0
 DB: Gaps: 0
 US-09-994-365-2 (1-136) x ABK6963 (1-3001)
 QY 19 GYITISerQlySerGlyGlyNH₂ProSerHisProProAlaGluAspArgGluAla 38
 DB 2205 GGATCTCAAGCAGCGAGGCGCACCCCTCTACCCACCCCAAGAGAGCCAGAGAGGCA 2264
 QY 39 GlySerProThrLeuProGlnGlyProProVal₁ProGlyAspProTTPProGlyAlaPro 58
 DB 2265 GGCTCCCAACATTGCTCTAGGGCCCCCACTGCCGTACCTTGCCAGGGGCAACC 2324
 QY 59 ProLeuPheGluAspProProProThrArgProSerArgProTTPArgAspLeuProGlu 78
 DB 2325 CCTCTCTTTGAAGATCCTCGGCTACCGGCCCAAGTGTCTCTGAGAGACCTGCTGAA 2384
 QY 79 ThrGlyVal₁TyrProProGlu₁ProProArgThrAspProProGlnProProArgProAsp 98
 DB 2385 ACTGGAGTCTGGCCCCCTGAACCGCTGAACGATCTCTCAACCTCCCGGCTGAC 2444
 QY 99 AspProTTPProAlaGlyProGlnInProProGluAsnProTTPProProAlaProGluVal 118
 DB 2445 GACCTTTGGCGGAGAGACCCCAAGCCCAAGAAACCCCTGCTGCTGCTGAGGTG 2504
 QY 119 AspAsnArgProGlnGluGluProAspLeuAspProProArgGluGluTyrArg 136
 DB 2505 GACAAACGAACTCTGAGAGAGACCACTAGACCAACCCCGGAGAGGTACAGA 2558

RESULT 5
 AAH45310
 ID AAH45310 standard; DNA; 25235 BP.
 XX
 AC AAH45310;
 XX
 DT 01-OCT-2001 (first entry)
 XX
 DE Human SEEK1 DNA.
 XX
 KW Human; MHC S; major histocompatibility complex S; vulgar psoriasis;
 KW diagnosis; primer; SEEK1; HCR; a-helix coiled-coil rod homologue;
 KW polymorphism; ds.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT exon 1..420
 FT /tag= a
 FT 421..1281
 FT /tag= b
 FT 1282..1405
 FT /tag= c
 FT /tag= d
 FT 1406..1601
 FT /tag= d
 FT 1602..1702
 FT /tag= e
 FT 1703..2351
 FT /tag= f
 FT 2352..2364
 FT /tag= g
 FT 2365..6286
 FT /tag= h
 FT 6287..6509
 FT /tag= i
 FT 6510..10416
 FT /tag= j
 FT 10417..10493
 FT /tag= k
 FT 10494..14243
 FT /tag= l
 FT 14244..14407
 FT /tag= m
 FT 14408..14243
 FT /tag= n
 FT 25190..25235
 FT /tag= o
 FT exon
 XX
 PN WO200142458-A1.
 XX
 PD 14-JUN-2001.
 XX
 PF 06-DEC-2000; 2000MO-JP008624.
 XX
 PR 06-DEC-1999; 99JP-00346867.
 XX
 PA (INOK/) INOKO H.
 XX
 PI Inoko H, Tamiya G;
 XX
 DR WPI; 2001-381680/40.
 XX
 PS New primer DNA, useful for detecting vulgar psoriasis.
 PS Claim 1; Page 46-62; 106pp; Japanese.
 CC The invention relates to a method of diagnosing vulgar psoriasis using
 CC primers based on the sequences of the human MHC S, SEEK1 and HCR genes.
 CC By analysing the sequences of these genes in Japanese patients with
 CC psoriasis and in normal subjects, it has been found that some of the
 CC examined polymorphisms correlate significantly to the group of patients
 CC with psoriasis. Vulgar psoriasis can therefore be diagnosed by analysing

CC these gene polymorphisms. The present sequence is the human SEEK1 gene
CC which was used to design primers for use in the invention

XX Sequence 25335 BP; 5967 A; 6703 C; 6487 G; 6078 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
Score:	2,13e-23	25335	118	0	0	0
Percent Similarity:	712.00					
Best Local Similarity:	100.00%					
Query Match:	88.12%					

DB: 4

US-09-994-365-2 (1-136) x AAH45310 (1-25235)

QY 19 GYIleSerGIySerGIyGluGlyHisProSerHisProProAlaGluAspArgGluGluAla 38

Db 1754 GGCATCTCAGAGCGAGCGGCGCACCCCTCTCACCCACCCGACGAGAGCGAGAGGCA 1813

QY 39 GYSerProThrIeuProGlnGlyProProValProGlyAspProTTPProGlyAlaPro 58

Db 1814 GGCCTCCCAACATGCTCTCAGGGCCCCCGAGTCCCGGTACCTTGCCAGGGGCAACC 1873

QY 59 ProIeuPheGluAspProProThraArgProSerArgProTTPArgAspIeuProGlu 78

Db 1874 CCTCTCTTGAAGATCCTCGCCTACCCGCGCAGTGTCTCTGAGAGACTGCTGAA 1933

QY 79 ThGlyValIleTTPProProGluProProArgThraAspProGlnProProArgProAsp 98

Db 1934 ACTGGAGTCTGGCCCCCTGAGACGCTGAGACGATCTCTCAACTCTCCGCGCTGAC 1993

QY 99 AspProTTPProAlaGlyProGlnProProGluAsnProTTPProProAlaProGluVal 118

Db 1994 GACCTTGGCGGGAGGAGACCCCGACGAGAAACCCCTGCTCTGCTGAGGTG 2053

QY 119 AspAsnArgProGlnGluGluProAspIeuAspProProArgGluGluYrarg 136

Db 2054 GACAAACGACCTCAGAGAGAGACCACTAGACCCCGGAGAGATACAGA 2107

RESULT 6

ABQ75680 ID ABQ75680 standard; DNA; 55050 BP.

XX AC ABQ75680;

DT 11-NOV-2002 (first entry)

XX DE Human SEEK1 consensus genomic DNA.

KW Human; SEEK1; chromosome 6p21; inflammatory disease; antiinflammatory;
antipsoaritic; gene therapy; gene; ds.

XX OS Homo sapiens.

XX PN WO200264831-A2.

PD 22-AUG-2002.

PF 13-FEB-2002; 2002WO-GB000653.

XX 13-FEB-2001; 2001GB-00003514.

PA (OXAG-) OXAGEN LTD.

XX Lench NJ, Allen MJ, Nicholas RK;

XX WPI; 2002-667013/71.

PT Polymorphisms in the SEEK1 gene and polymucleotides encoding the SEEK1
PT gene, for treating, diagnosing or determining susceptibility to SEEK1
PT mediated disease, e.g. inflammatory disease such as psoriasis.

XX Claim 4; Fig 2; 69pp; English.

XX The present invention describes a polymucleotide (I) comprising: (a) a
CC nucleic acid sequence (II) encoding the SEEK1 gene; or (b) a nucleic acid
CC sequence (III) encoding a fragment of the SEEK1 gene; or (c) a nucleic
CC acid sequence (IV) that hybridises under stringent conditions to the
CC polymucleotide of (II) or (III). (I) has antiinflammatory and
CC antipsoaritic activities and can be used in gene therapy. The alleles of
CC one or more polymorphisms in the SEEK1 gene can be used for the
CC manufacture of a medicament for the diagnosis and treatment of SEEK1
CC mediated disease. SEEK1 protein fragments are useful in diagnostic,
CC prognostic or therapeutic methods, or as research tools in drug
CC screening. Human SEEK1 is located to chromosome 6p21. The present
CC sequence represents a human SEEK1 nucleotide sequence

XX Sequence 55050 BP; 13076 A; 14198 C; 14560 G; 13197 T; 0 U; 19 Other;

Alignment Scores:

Pred. No.:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
Score:	3,92e-23	55050	118	0	0	0
Percent Similarity:	712.00					
Best Local Similarity:	100.00%					
Query Match:	88.12%					

DB: 6

US-09-994-365-2 (1-136) x ABQ75680 (1-55050)

QY 19 GYIleSerGIySerGIyGluGlyHisProSerHisProProAlaGluAspArgGluGluAla 38

Db 27099 GGCATCTCAGAGCGAGCGGCGCACCCCTCTCACCCACCCGACGAGAGCGAGAGGCA 27158

QY 39 GYSerProThrIeuProGlnGlyProProValProGlyAspProTTPProGlyAlaPro 58

Db 27159 GGCCTCCCAACATGCTCTCAGGGCCCCCGAGTCCCGGTACCTTGCCAGGGGCAACC 27218

QY 59 ProIeuPheGluAspProProThraArgProSerArgProTTPArgAspIeuProGlu 78

Db 27219 CCTCTCTTGAAGATCCTCGCCTACCCGCGCAGTGTCTCTGAGAGACTGCTGAA 27278

QY 79 ThGlyValIleTTPProProGluProProArgThraAspProGlnProProArgProAsp 98

Db 27279 ACTGGAGTCTGGCCCCCTGAGACGCTGAGACGATCTCTCAACTCTCCGCGCTGAC 27338

QY 99 AspProTTPProAlaGlyProGlnProProGluAsnProTTPProProAlaProGluVal 118

Db 27339 GACCTTGGCGGGAGGAGACCCCGACGAGAAACCCCTGCTCTGCTGAGGTG 27398

QY 119 AspAsnArgProGlnGluGluProAspIeuAspProProArgGluGluYrarg 136

Db 27399 GACAAACGACCTCAGAGAGAGACCACTAGACCCCGGAGAGATACAGA 27452

RESULT 7

ACH72505 ID ACH72505 standard; DNA; 565 BP.

XX AC ACH72505;

DT 29-JUL-2004 (first entry)

XX DE Human genome derived single exon probe #5700.

KW Human; probe; ss; gene expression; single exon probe; microarray;
alternative splicing event; genomic alteration.

XX OS Homo sapiens.

XX PN US2003194704-A1.

PD 16-OCT-2003.

PF 03-APR-2002; 2002US-00029386.

XX 03-APR-2002; 2002US-00029386.

XX 03-APR-2002; 2002US-00029386.

XX

XX

XX

XX

XX

PA (PENN/) PENN S G.
 PA (RANK/) RANK D R.
 PA (HANK/) HANZEL D K.
 PI Penn SG, Rank DR, Hanzel DK;
 XX WPI; 2004-119264/12.
 XX
 PT New human genome-derived single exon nucleic acid probes useful for human
 PT gene expression analysis, for identifying or characterizing alternative
 PT splicing events, for assessing genomic alterations or as tools for
 PT surveying tissues.
 PS
 PS Claim 15; SEQ ID NO 5700; 80pp; English.
 XX
 CC The invention relates to a nucleic acid probe for measuring human gene
 CC expression, comprising any of the 27,400 fully defined nucleotide
 CC sequences in the specification, or their complements or fragments, and
 CC encoding at least 8 amino acids of any of the 6888 amino acid sequences
 CC fully defined in the specification. The probe is a single exon probe that
 CC hybridizes under high stringency conditions to a nucleic acid molecule
 CC expressed in human cells or tissues. Also included are a spatially-
 CC addressable set of single exon nucleic acid probes for measuring human
 CC gene expression (comprising a plurality of single exon nucleic acid
 CC probes cited above, where each of the plurality of probes is separately
 CC and addressably isolatable or amplifiable from the plurality), a single
 CC exon microarray for measuring human gene expression, a method of
 CC measuring human gene expression, a vector comprising the single exon
 CC probe cited above, an ORF-encoded peptide comprising at least 8
 CC contiguous amino acids of any of the above-mentioned amino acid
 CC sequences (optionally with conservative amino acid substitutions), an
 CC isolated antibody that binds specifically to a peptide cited above,
 CC methods of selling and/or licensing single exon probes or microarrays to
 CC a customer desiring to measure gene expression, a method of providing
 CC human gene expression data by subscription, and a computer-readable
 CC storage medium which contains a database having a plurality of records
 CC (each record including data on the expression of a single exon probe
 CC cited above. The probe, methods and apparatus are useful in gene
 CC expression analysis. The probes may be used as tools for surveying
 CC tissues to detect the presence of expressed messages that contain their
 CC specific exon, or in constructing genome-derived single exon microarrays.
 CC In addition, the probes are used in identifying and characterizing
 CC alternative splicing events, in detecting and characterizing gross
 CC alterations in the genomic locus that includes their exon, in assessing
 CC smaller genomic alterations, in printing the synthesis of nucleic acids,
 CC or in expressing the ORF-encoded peptide. The present sequence is a human
 CC single exon probe of the invention. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from USPTO at
 CC seqdata.uspto.gov/sequence.html?docid=20030194704
 CC
 XX
 SQ Sequence 565 BP; 99 A; 227 C; 112 G; 127 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 2,03e-14 Length: 565
 Score: 486.00 Matches: 79
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 60.15% Indels: 0
 DB: 12 Gaps: 0
 US-09-994-365-2 (1-136) x ACH72505 (1-565)
 QY 58 ProProLeuPheGluAaPProProProThArGProSeArGProTPaGAPleuPro 77
 Db 1 CCCCTCTCTTGAAGAATCCCTCCGCTACCGCCCGCCAGTCGTCCCTGAGAGACTGCT 60
 QY 78 GluThrcGlyValTPProProGluProProArGhArPProPProGInProPProArGPro 97
 Db 61 GAAACCTGAGCTGGCCCGCCGAAACCGCTAGAAAGGATCTCTCAACCTCCCGGACT 120
 QY 98 AspAaPProTPProAlaGlyProGInProProGluAaPProTPProProAlaPProGlu 117

Db 121 GAGACCCCTTGCCGCGAGAGACCCAGCCCCAGAAAACCCCTGGCCCTCTGCCCCCTGAG 180
 QY 118 ValAspAaPProTPProGInGluProProAaPleuAaPProProArGInGluYrArG 136
 Db 181 GTGAGCAACCGACTCTAGAGAGAGCCAGACTTAGACCTACCCCGGAGAGTACAG 237
 RESULT 8
 ACH86315
 ID ACH86315 standard; DNA; 157 BP.
 XX
 AC ACH86315;
 XX
 DT 29-JUL-2004 (first entry)
 XX
 DE Human genome derived single exon probe #19510.
 XX
 KW Human, probe; ss; gene expression; single exon probe; microarray;
 KW alternative splicing event; genomic alteration.
 XX
 OS Homo sapiens.
 XX
 PN US2003194704-A1.
 XX
 PD 16-OCT-2003.
 XX
 PF 03-APR-2002; 2002US-00029386.
 XX
 PR 03-APR-2002; 2002US-00029386.
 XX
 PA (PENN/) PENN S G.
 PA (RANK/) RANK D R.
 PA (HANK/) HANZEL D K.
 PI Penn SG, Rank DR, Hanzel DK;
 XX WPI; 2004-119264/12.
 XX
 PT New human genome-derived single exon nucleic acid probes useful for human
 PT gene expression analysis, for identifying or characterizing alternative
 PT splicing events, for assessing genomic alterations or as tools for
 PT surveying tissues.
 PS
 PS Claim 1; SEQ ID NO 19510; 80pp; English.
 XX
 CC The invention relates to a nucleic acid probe for measuring human gene
 CC expression, comprising any of the 27,400 fully defined nucleotide
 CC sequences in the specification, or their complements or fragments, and
 CC encoding at least 8 amino acids of any of the 6888 amino acid sequences
 CC fully defined in the specification. The probe is a single exon probe that
 CC hybridizes under high stringency conditions to a nucleic acid molecule
 CC expressed in human cells or tissues. Also included are a spatially-
 CC addressable set of single exon nucleic acid probes for measuring human
 CC gene expression (comprising a plurality of single exon nucleic acid
 CC probes cited above, where each of the plurality of probes is separately
 CC and addressably isolatable or amplifiable from the plurality), a single
 CC exon microarray for measuring human gene expression, a method of
 CC measuring human gene expression, a vector comprising the single exon
 CC probe cited above, an ORF-encoded peptide comprising at least 8
 CC contiguous amino acids of any of the above-mentioned amino acid
 CC sequences (optionally with conservative amino acid substitutions), an
 CC isolated antibody that binds specifically to a peptide cited above,
 CC methods of selling and/or licensing single exon probes or microarrays to
 CC a customer desiring to measure gene expression, a method of providing
 CC human gene expression data by subscription, and a computer-readable
 CC storage medium which contains a database having a plurality of records
 CC (each record including data on the expression of a single exon probe
 CC cited above. The probe, methods and apparatus are useful in gene
 CC expression analysis. The probes may be used as tools for surveying
 CC tissues to detect the presence of expressed messages that contain their
 CC specific exon, or in constructing genome-derived single exon microarrays.
 CC In addition, the probes are used in identifying and characterizing
 CC alternative splicing events, in detecting and characterizing gross
 CC alterations in the genomic locus that includes their exon, in assessing

CC smaller genomic alterations, in priming the synthesis of nucleic acids,
CC or in expressing the ORF-encoded peptide. The present sequence is a human
CC single exon probe of the invention. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?DocId=20030194704
XX

Sequence 157 BP; 38 A; 64 C; 38 G; 17 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	4,85e-07	Length:	157
Score:	314.00	Matches:	51
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	38.86%	Indels:	0
DB:	12	Gaps:	0

US-09-994-365-2 (1-136) x ACH6315 (1-157)

QY 86 ProProArgThraSPProGlnProProArgProAspProTrpProAlaGlyPro 105

Db 2 CCGCTAGAGACGATCCTCTCAACCTCCCGGCTGACGACCTTGCGCGAGAGACC 61

QY 106 GlnProProGluAsnProTrpProProAlaProGluValAspAsnArgProGlnGlu 125

Db 62 CAGCCCCAGAAAAACCTGCTGCTGCTGCTGCTGAGTGAGCAACGACCTCAGAGAG 121

QY 126 ProAspLeuAspProProArgGluGluTrpArg 136

Db 122 CCAAGCTTAGACCAACCCCGGAGAGATACAGA 154

RESULT 9

ACA43990/c
ID ACA43990 standard; DNA; 711 BP.

XX ACA43990;

XX 19-JUN-2003 (first entry)

XX Prokaryotic essential gene #25647.

XX Antisense; ds; prokaryotic essential gene; cell proliferation;

XX drug design; gene.

XX Pseudomonas putida.

XX WO200277183-A2.

XX 03-OCT-2002.

XX 21-MAR-2002; 2002WO-US009107.

XX 21-MAR-2001; 2001US-00815242.

XX 06-SEP-2001; 2001US-00948893.

XX 25-OCT-2001; 2001US-0342923P.

XX 08-FEB-2002; 2002US-00072851.

XX 06-MAR-2002; 2002US-0362699P.

XX (ELIT-) ELITRA PHARM INC.

XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;

XX Wall D, Trivick JD, Carr GD, Yamamoto R, Forsyth RA, Xu HH;

XX WPI; 2003-029926/02.

XX P-FSDB; ABU40120.

XX New antisense nucleic acids, useful for identifying proteins or screening
XX PT for homologous nucleic acids required for cellular proliferation to
XX PT isolate candidate molecules for rational drug discovery programs.
XX PS Claim 14; SEQ ID NO 31860; 1766pp; English.
XX The invention relates to an isolated nucleic acid comprising any one of

CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is one of the target
CC prokaryotic essential genes. Note: The sequence data for this patent did
CC not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pat_sequences
XX

Sequence 711 BP; 120 A; 161 C; 304 G; 126 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	0.264	Length:	711
Score:	199.00 <td>Matches:</td> <td>46</td>	Matches:	46
Percent Similarity:	44.95% <td>Conservative:</td> <td>3</td>	Conservative:	3
Best Local Similarity:	42.20% <td>Mismatches:</td> <td>42</td>	Mismatches:	42
Query Match:	24.63% <td>Indels:</td> <td>18</td>	Indels:	18
DB:	8 <td>Gaps:</td> <td>6</td>	Gaps:	6

US-09-994-365-2 (1-136) x ACA43990 (1-711)

QY 27 ProSerHisProFroAlaGluAspArgGluAlaGlySerProThrLeuProGlnGly 46

Db 446 CCGGATGGCGCACCG-----TCACCGCGCTGCGG---TGG 411

QY 47 ProProValPro---GlyAspProTrpProGlyAlaProProLeuHeuGluAspProPro 65

Db 410 CCACCACTTCGCTCCGCCACCATGACCGCGCCACCACTT-----CCACCA 357

QY 66 ProThrArgProSerArgProTrpArgAspLeuProGluThrGlyValTrpProGlu 85

Db 356 CCGTGGCCACACACCGCGCGCTTCCACCAACCAACG-----TGGCCACCGCA 309

QY 86 ProProArgThraSP-----ProProGlnProProArgProAspAspProTrpPro 102

Db 308 CCGCGCTTCCACCAACCGATGACCGCGCGCGCTTCCACCGCGCGCGATGACCA 249

QY 103 AlaGlyProGlnProProGluAsnProTrpProProAlaProGluValAspAsnArgPro 122

Db 248 CCGCGCGCGCGCTTCCACCGCGCGATGACCGCGCGCGCGCGCGCGCGCGCGCGCG 189

QY 123 GlnGluGluProAspLeuAspProPro 131

Db 188 TGGCCACCG 162

RESULT 10

ACA40420/c
ID ACA40420 standard; DNA; 2772 BP.

XX ACA40420;

XX

DT	19-JUN-2003	(first entry)
XX		
DE	Prokaryotic essential gene #22077.	
XX		
KW	Antisense, ds, prokaryotic essential gene; cell proliferation;	
KW	drug design; gene.	
XX		
OS	Mycobacterium tuberculosis.	
XX		
PN	WO200271763-A2.	
XX		
XX	03-OCT-2002.	
PD		
PF	21-MAR-2002; 2002WO-US009107.	
XX		
PR	21-MAR-2001; 2001US-00815242.	
PR	06-SEP-2001; 2001US-00948993.	
PR	25-OCT-2001; 2001US-0342923P.	
PR	08-FEB-2002; 2002US-00072851.	
PR	06-MAR-2002; 2002US-0362699P.	
XX		
PA	(ELIT-) ELITRA PHARM INC.	
XX		
PI	Wang L, Zamudio C, Malone C, Haseelbeck R, Ohlsen KU, Zyskind JW;	
PI	Wall D, Travick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;	
XX		
XX	WPI; 2003-029926/02.	
DR	P-PSDB; ABU36550.	
XX		
PT	New antisense nucleic acids, useful for identifying proteins or screening	
PT	for homologous nucleic acids required for cellular proliferation to	
PT	isolate candidate molecules for rational drug discovery programs.	
PS		
XX	Claim 14; SEQ ID NO 28290; 1766bp; English.	
XX		
CC	The invention relates to an isolated nucleic acid comprising any one of	
CC	the 6213 antisense sequences given in the specification where expression	
CC	of the nucleic acid inhibits proliferation of a cell. Also included are:	
CC	(1) a vector comprising a promoter operably linked to the nucleic acid	
CC	encoding a polypeptide whose expression is inhibited by the antisense	
CC	nucleic acid; (2) a host cell containing the vector; (3) an isolated	
CC	polypeptide or its fragment whose expression is inhibited by the	
CC	antisense nucleic acid; (4) an antibody capable of specifically binding	
CC	the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular	
CC	proliferation or the activity of a gene in an operon required for	
CC	proliferation; (7) identifying a compound that influences the activity of	
CC	the gene product or that has an activity against a biological pathway	
CC	required for proliferation, or that inhibits cellular proliferation; (8)	
CC	identifying a gene required for cellular proliferation or the biological	
CC	pathway in which a proliferation-required gene or its gene product lies	
CC	or a gene on which the test compound that inhibits proliferation of an	
CC	organism acts; (9) manufacturing an antibiotic; (10) profiling a	
CC	compound's activity; (11) a culture comprising strains in which the gene	
CC	product is overexpressed or underexpressed; (12) determining the extent	
CC	to which each of the strains is present in a culture or collection of	
CC	strains; or (13) identifying the target of a compound that inhibits the	
CC	proliferation of an organism. The antisense nucleic acids are useful for	
CC	identifying proteins or screening for homologous nucleic acids required	
CC	for cellular proliferation to isolate candidate molecules for rational	
CC	drug discovery programs, or for screening homologous nucleic acids	
CC	required for proliferation in cells other than <i>S. aureus</i> , <i>S. typhimurium</i> ,	
CC	<i>K. pneumoniae</i> or <i>P. aeruginosa</i> . The present sequence is one of the target	
CC	prokaryotic essential genes. Note: The sequence data for this patent did	
CC	not form part of the printed specification, but was obtained in	
CC	electronic format directly from WIPO at	
CC	ftp.wipo.int/pub/published_pct_sequences	
XX		
SO	Sequence 2772 BP; 397 A; 904 C; 1108 G; 363 T; 0 U; 0 Other;	
Alignment Scores:		
Score:	0.805	Length: 2772
Score:	198.50	Match:
Percent Similarity:	32.54%	Conservative: 4

Best Local Similarity:	30.18%	Mismatches:	45
Query Match:	24.57%	Indels:	69
DB:	8	Gaps:	6

US-09-994-365-2 (1-136) x ACA40420 (1-2772)

```

QY      27   ProSerHisProProlAGluAapArgGluGluAlaGlySerProThrLeuProGlnGly 46
          ||| ||||| ||||| ||| ||| :||| ||| |||
Dd      1115 CCGCCGATGCCGGCCCCGGCGCGCTGCCGCCGCCTCGCCGCCGCCCAACGCCG 1056
           ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      47   ProProValProGluAapProTrpProGlyAlaProFleuPhaeGluAapPro----- 64
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Dd      1055 CCAACTACGGCGGGCGCGCCTTGGCGCGCGTCGCGCGCGCCACCAGCACCTGAGCTG 996
           ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      65   -----ProProThraArgProSerArg 71
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Dd      995 CCGCCGATCCACCCCGCGAACCAACGATCCCGCGCGCGCGCGCTCCCCTGTGCGCG 936
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      72   ProHrp-----ArgAapLeuPro 77
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Dd      935 CCCCTGGCGCGCTTGCTCATCAATGCCGACCGTAGTCCCTCAGCGCGCCAGCCGTGTCCG 876
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      78   GluThrGlyValTrpProProGluAapProArgThrAsp----- 90
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Dd      875 CCAGACCGCGCCCTGTGCCACCCATGCGCGGTACCGCATCGCGTTGATTCCCCCGTGG 816
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      91   -----ProProGlnPro 94
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Dd      815 CCGAAACAAGCCGAGCGCGTGGCGCGACCCCGCGCGCGCGCGCATGCCGCCGATGCC 756
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      95   ProArgProAapAspProTrpProAlaGly----- 104
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Dd      755 CCGATGTCCGCGCGTGGCG--CCGGCGGAGCCGGACAGTCGCCGCGCGCCGTGCCG 699
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      105   -----ProGlnProProGluAapProTrpProProAlaProGluValAapAsnArg 121
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Dd      698 CCGAGACGCCCCCAAGATCCGCGGAGACCACTTGAGCGCGGACACCACTGTG----- 648
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      122   ProGlnGluLupProAapLeuAspPro 130
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Dd      647 CCGAATAGCAGGCCCGCGCTTGGCGCGG 621
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

RESULT 11
AAI99682_10/c
Continuation (11 of 45) of AAI99682 from base 100001 (Mycobacterium tuberculosis strain
WP Sequence split into 45 fragments LOCUS AAI99682 Accession AAI99682
WP Fragment Name Begin End
WP AAI99682_01 1 110000
WP AAI99682_01 100001 110000
WP AAI99682_02 200001 310000
WP AAI99682_03 300001 410000
WP AAI99682_04 400001 510000
WP AAI99682_05 500001 610000
WP AAI99682_06 600001 710000
WP AAI99682_07 700001 810000
WP AAI99682_08 800001 910000
WP AAI99682_09 900001 1010000
WP AAI99682_10 1000001 1110000
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WP AAI99682_19 1900001 2010000
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WP AAI99682_21 2100001 2210000
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WP AAI99682_23 2300001 2410000
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WP AAI99682_25 2500001 2610000

Db 91242 CGAGCAGCGCCCTTGCCACCCATGCCCGGTACCGCCATGCCGTTGATTTCCCCCGTGG 91183

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QY 91 -----ProProGlnPro 94
Db 91182 CCGAACAACCCGAGCCGTGCGCCGACCCCGCCGCCGAGATCCGCGATGCC 91123
QY 95 ProArgProAspAspProTTPProAlaGly-----104
Db 91122 CCGATGCGCCGCGTCCG---CCGGCGGAGACCGGACCCATGCCGCGCCGCGTCCG 91066
QY 105 -----ProGlnProGluAsnProTTPProAlaProGluValAspAsnArg 121
Db 91065 CCGAGAGCCCGCAAGTCCGCGGAGCCACCTGCGCGCGGACACCGCTTG-----91015
QY 122 ProGlnGluGluProAspLeuAspPro 130
Db 91014 CCGAATAGCAGCCGCGCTTGCCGCGC 90988

RESULT 13
AA123276/c
ID AA123276 standard; DNA; 446 BP.
AC AA123276;
XX
DT 12-OCT-2001 (first entry)
XX
DE Probe #13209 for gene expression analysis in human cervical cell sample.
XX
KM Probe: human; microarray; gene expression; cervical epithelial cell;
XX cervical cancer; ss.
XX Homo sapiens.
XX
PN WO200157278-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US000670.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI; 2001-488901/53.
XX
DR Human genome-derived single exon nucleic acid probes useful for analyzing
XX gene expression in human cervical epithelial cells.
XX
PT Claim 25; SEQ ID NO 13209; 487bp; English.
XX
PS The present invention relates to human single exon nucleic acid probes
XX (SENPs). The present sequence is one such probe. The SENPs are derived
XX from human Hela cells. The SENPs can be used to produce a single exon
XX microarray, which can be used for measuring human gene expression in a
XX sample derived from human cervical epithelial cells. By measuring gene
XX expression, the probes are therefore useful in grading and/or staging of
XX diseases of the cervix, notably cervical cancer. Note: The sequence data
XX for this patent did not form part of the printed specification, but was
XX obtained in electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 446 BP; 31 A; 26 C; 254 G; 135 T; 0 U; 0 Other;
XX
Alignment Scores:
Pred. No.: 0.265 Length: 446
Score: 195.50 Matches: 46
Percent Similarity: 40.32% Conservative: 4
XX

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Best Local Similarity: 37.10% Mismatches: 64
Query Match: 24.20% Indels: 10
DB: 4 Gaps: 2
US-09-994-365-2 (1-136) x AA123276 (1-446)
QY 14 CysLeuHisThrArg-GlyTleSerGlySerGluGlyHisProSerHisProAlaG1 33
Db 443 TGCACGACAGCAAAATATATCTACGACACACACACACACACACACACACACACATC 384
QY 33 uAPArgGluGluAlaGlySerProThrLeuProGlnGlyProProValProGlyAspPr 53
Db 383 ACCACACACACACACACACATCCACACACACACACACACATCCACACACATCACC 324
QY 53 oTTPProGlyAlaProProLeuPheGluAspProProProThrArgProSerArgProTr 73
Db 323 ACCACACACACACACACACATCCACACACACACACACACACACACACACATCACC 264
QY 73 PARGAspLeuProGluThrGlyValTTPProProGluProProArgThrAspProProG1 93
Db 263 ACCATCATCACACCA-----CCACACACACACACACACATCACACACACACACC 216
QY 93 nProProArgProAspAspProTTPProAlaGlyProGlnProProGluAsnProTTPPr 113
Db 215 ACCACACACACACATCACACACACACACACACATCCATCCACACACACACATCACC 156
QY 113 o-----ProAlaProGluValAspAsnArgProGlnGluGluProAspLe 128
Db 155 ATCATCACACCACTCACCGCCACCATCATCCATCACACACACCGCGCACCATCCACT 96
QY 128 uAspProPro 131
Db 95 GCCACCGCCA 86

RESULT 14
ABA68382/c
ID ABA68382 standard; DNA; 446 BP.
XX
XX ABA68382;
XX
DT 01-FEB-2002 (first entry)
XX
DE Human foetal liver single exon nucleic acid probe #16687.
XX
XX Human; foetal liver; gene expression; single exon nucleic acid probe; ss.
XX
XX Homo sapiens.
XX
XX WO200157277-A2.
XX
XX PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US000669.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI; 2001-483447/52.
XX
DR Human genome-derived single exon nucleic acid probes useful for analyzing
XX gene expression in human fetal liver.
XX
PT Claim 4; SEQ ID NO 16687; 639bp + Sequence Listing; English.
XX
XX

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OM nucleic - nucleic search, using sw model

Run on: January 11, 2005, 08:16:10 ; Search time 4026 Seconds
(without alignments)
10465.753 Million cell updates/sec

Title: US-09-994-365-1

Perfect score: 891
Sequence: 1 ccccttcgggggtccccagca.....taaaatcatgtcttctta 891

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 4526729 seqs, 23644849745 residues

Word size : 0

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

GenBml:.*
1: gb_ha:.*
2: gb_hcg:.*
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9: gb_pr:.*
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11: gb_sts:.*
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13: gb_un:.*
14: gb_vi:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	891	100.0	891	6	AX477387 Sequence
2	840	94.3	1143	6	CO722444 Sequence
3	840	94.3	1185	9	AR484420 Homo sapi
4	828	92.9	1473	6	AX406002 Sequence
5	781	87.7	1143	9	AB031480 Homo sapi
6	775	87.0	2997	6	AX477396 Sequence
7	775	87.0	3001	6	AX477390 Sequence
8	775	87.0	40878	9	AC004195 Homo sapi
9	728	81.7	113388	9	AL773544 Human DNA
10	724	81.3	25235	6	BD095297 The metho
11	724	81.3	30911	9	AB088114 Homo sapi
12	724	81.3	39196	9	AB023060 Homo sapi
13	724	81.3	55050	6	AX522117 Sequence
14	724	81.3	70288	9	AL662867 Human DNA
15	724	81.3	98999	9	AP000510 Homo sapi
16	724	81.3	135396	9	BA927139 Human DNA
17	622	69.8	204298	9	AL662844 Human DNA
18	269	30.2	300050	9	AB100083 Pan trogl
19	119	13.4	168887	9	AL662833 Human DNA

C 20	117	13.1	175689	9	AC148703	AC148703 Macaca mu
C 21	94	10.5	200068	9	AC148691	AC148691 Macaca mu
C 22	87	9.8	248	6	AR418279	AR418279 Sequence
C 23	87	9.8	248	6	AX978973	AX978973 Sequence
C 24	87	9.8	248	6	BD113832	BD113832 EST and e
C 25	60	6.7	60	6	CQ535442	CQ535442 Sequence
C 26	54	6.1	388	9	HS144A35	U18174 Human HLA C
C 27	41	4.6	306	9	HS144A32	U18171 Human HLA C
C 28	38	4.3	773	10	AF159091	AF159091 Mus muscu
C 29	38	4.3	809	10	AF484421	AF484421 Mus muscu
C 30	38	4.3	1377	10	AF159090	AF159090 Mus muscu
C 31	38	4.3	159179	10	MMHC322F16	AF111103 Mouse maj
C 32	38	4.3	226594	10	AC087216	U18163 Human HLA C
C 33	33	3.7	250	9	HS144A26	AX344554 Sequence
C 34	33	3.7	349980	6	AX344554	AX344554 Sequence
C 35	28	3.1	343	9	HS144A31	U18170 Human HLA C
C 36	26	2.9	204	6	AX911909	AX911909 Sequence
C 37	26	2.9	204	6	BD047442	BD047442 Sus scrofa
C 38	26	2.9	383	4	AF484422	AF484422 Sus scrofa
C 39	26	2.9	154749	4	AB113354	AB113354 Sus scrofa
C 40	22	2.5	147524	2	AC069201	AC069201 Homo sapi
C 41	22	2.5	159479	2	AC074352	AC074352 Homo sapi
C 42	22	2.5	159705	2	AC092928	AC092928 Homo sapi
C 43	22	2.5	160042	2	AL365211	AL365211 Homo sapi
C 44	22	2.5	167152	9	AC092939	AC092939 Homo sapi
C 45	22	2.5	175968	9	AC018684	AC018684 Homo sapi

ALIGNMENTS

RESULT 1	AX477387	Sequence 1 from Patent WO0244375.	891 bp	DNA	linear	PAT 12-AUG-2002
LOCUS	AX477387					
DEFINITION	AX477387					
ACCESSION	AX477387.1	GI:22216617				
VERSION						
KEYWORDS						
SOURCE						
ORGANISM						
	Homo sapiens (human)					
	Homo sapiens					
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.					

REFERENCE	1	Charmley, P., Moss, P. and Mceuen, M.
AUTHORS		
TITLE		Compositions and methods for diagnosing or treating psoriasis
JOURNAL		Patent: WO 024375-A 1 06-JUN-2002;
CELL		Celltech R & D, Inc. (US)
FEATURES		Location/Qualifiers
source		1..891
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		/mol_type="unassigned DNA"
		/db_xref="taxon:9606"
		64..474
		/note="unassigned protein product"
		/codon_start=1
		/protein_id="CAD3680.1"
		/db_xref="GI:22216618"
		/translation="MILNKLGLIVLCIHTRGISGSRGHPSPADREAGPTLP
		QGPVPDPPWGAAPLEFEDPPTRPSRWDLPETGVWPPSPPTDPPQPRDPPW
		AGPQPPNPMPAPAEVNDPQEBDDLPREYR"

CDS

ORIGIN	
Query Match	100.0%; Score 891, DB 6, length 891
Best Local Similarity	100.0%; Pred. No. 0;
Matches	891; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	CCCTCTGGGGTCCACGACCCAGACTCAGCCAGCCAGCTTTGGGGGCGAGTACATA	60
Db	1	CCTCTGGGGTCCACGACCCAGACTCAGCCAGCTTTGGGGGCGAGTACATA	60
Qy	61	GCCATGATCTCTCACTGAAGCTCTGGGATCTGTCTTGGCTGCACACCAAGGC	120
Db	61	GCCATGATCTCTCACTGAAGCTCTGGGATCTGTCTTGGCTGCACACCAAGGC	120

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QY 121 ATCTCAGGACGAGGAGGACACCCCTCTCAACCAACCCGAGAGACGAGAGGAGGACAGG 180
DB 121 ATCTCAGGACGAGGAGGAGGACACCCCTCTCAACCAACCCGAGAGACGAGAGGAGGACAGG 180
QY 181 TCCCAACATTTGCTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 240
DB 181 TCCCAACATTTGCTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 240
QY 241 CTCTTGAAGATCTCTCCGCTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 300
DB 241 CTCTTGAAGATCTCTCCGCTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 300
QY 301 GAGAGTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 360
DB 301 GAGAGTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 360
QY 361 CTTTGGCCGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 420
DB 361 CTTTGGCCGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 420
QY 421 AACGAGCTCAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 480
DB 421 AACGAGCTCAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 480
QY 481 CCCTCAGCCGCTCTGTTCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 540
DB 481 CCCTCAGCCGCTCTGTTCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 540
QY 541 TCCCGGTAATTTCTTCCCAATTTAGCCATTTAGCCATTTAGCCATTTAGCCATTTAGCCATTT 600
DB 541 TCCCGGTAATTTCTTCCCAATTTAGCCATTTAGCCATTTAGCCATTTAGCCATTTAGCCATTT 600
QY 601 TTTATTTGTAACCCGTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 660
DB 601 TTTATTTGTAACCCGTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 660
QY 661 CTTAGTCTCAGATCGCCGCTTTTCTCTGACAGGCTTAAAGCTTAAAGCTTAAAGCTTAAAGCTT 720
DB 661 CTTAGTCTCAGATCGCCGCTTTTCTCTGACAGGCTTAAAGCTTAAAGCTTAAAGCTTAAAGCTT 720
QY 721 CTCAGAGGCTCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 780
DB 721 CTCAGAGGCTCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 780
QY 781 CAGGAGCTATGATCTGTGTTCCCTTCTGACAGGCTTAAAGCTTAAAGCTTAAAGCTTAAAGCT 840
DB 781 CAGGAGCTATGATCTGTGTTCCCTTCTGACAGGCTTAAAGCTTAAAGCTTAAAGCTTAAAGCT 840
QY 841 AGACAGCTGTGCTTCCATGAAACGAAAAATTAATCATGTTTCTTAA 891
DB 841 AGACAGCTGTGCTTCCATGAAACGAAAAATTAATCATGTTTCTTAA 891

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RESULT 2
CQ722444 1143 bp DNA linear PAT 03-FEB-2004
LOCUS Sequence 8378 from Patent WO02068579.
DEFINITION CQ722444
ACCESSION CQ722444
VERSION CQ722444.1 GI:42283301
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

```

```

REFERENCE
AUTHORS Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.
TITLE Kites, such as nucleic acid arrays, comprising a majority of
numanexons or transcripts, for detecting expression and other uses
theroeof
JOURNAL Patent: WO 02068579-A 8378 06-SBP-2002;
PB Corporation (NY) (US)
FEATURES Location/Qualifiers

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source 1..1143
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

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Query Match 94.3%; Score 840; DB 6; Length 1143;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 890; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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ORIGIN
QY 1 CTCTTGGGAGTTCACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 60
DB 253 CTTTGGGAGTTCACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 312
QY 61 GCCATGATCTCTCAACTGGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 120
DB 313 GCCATGATCTCTCAACTGGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 372
QY 121 ATCTCAGGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 180
DB 373 ATCTCAGGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 432
QY 181 TCCCAACATTTGCTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 240
DB 433 TCCCAACATTTGCTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 492
QY 241 CTCTTGAAGATCTCTCCGCTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 300
DB 493 CTCTTGAAGATCTCTCCGCTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 552
QY 301 GAGAGTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 360
DB 553 GAGAGTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 612
QY 361 CTTTGGCCGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 420
DB 613 CTTTGGCCGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 672
QY 421 AACGAGCTCAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 480
DB 673 AACGAGCTCAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 732
QY 481 CCCTCAGCCGCTCTGTTCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 540
DB 733 CCCTCAGCCGCTCTGTTCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 792
QY 541 TCCCGGTAATTTCTTCCCAATTTAGCCATTTAGCCATTTAGCCATTTAGCCATTTAGCCATTT 600
DB 793 TCCCGGTAATTTCTTCCCAATTTAGCCATTTAGCCATTTAGCCATTTAGCCATTTAGCCATTT 852
QY 601 TTTATTTGTAACCCGTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 660
DB 853 TTTATTTGTAACCCGTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 912
QY 661 CTTAGTCTCAGATCGCCGCTTTTCTCTGACAGGCTTAAAGCTTAAAGCTTAAAGCTTAAAGCTT 720
DB 913 CTTAGTCTCAGATCGCCGCTTTTCTCTGACAGGCTTAAAGCTTAAAGCTTAAAGCTTAAAGCTT 972
QY 721 CTCAGAGGCTCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 780
DB 973 CTCAGAGGCTCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1032
QY 781 CAGGAGCTATGATCTGTGTTCCCTTCTGACAGGCTTAAAGCTTAAAGCTTAAAGCTTAAAGCT 840
DB 1033 CAGGAGCTATGATCTGTGTTCCCTTCTGACAGGCTTAAAGCTTAAAGCTTAAAGCTTAAAGCT 1092
QY 841 AGACAGCTGTGCTTCCATGAAACGAAAAATTAATCATGTTTCTTAA 891
DB 1093 AGACAGCTGTGCTTCCATGAAACGAAAAATTAATCATGTTTCTTAA 1143

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RESULT 3
AF484420

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LOCUS AF484420 1185 bp mRNA linear PRI 02-MAR-2003
DEFINITION Homo sapiens psoriasis susceptibility 1 candidate 2 (PSORS1C2)
ACCESSION AF484420
VERSION AF484420.1 GI:28628834
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Euteleostomi; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 1185)
Holm,S.J., O'Brien,K.P., Carlen,L. and Stahle-Backdahl,M.
The PSORS1C1 and PSORS1C2 genes in 6p21.3 associate strongly with
psoriasis in the Swedish population
JOURNAL Unpublished
AUTHORS 2 (bases 1 to 1185)
Holm,S.J., O'Brien,K.P., Carlen,L. and Stahle-Backdahl,M.
TITLE Direct Submission
JOURNAL Submitted (15-FEB-2002) Dermatology, Karolinska Institute, L8:02
Karolinska Stjukhuset, Stockholm S-17176, Sweden
FEATURES
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Best Local Similarity 99.9%; Pred. No. 0;
Matches 890; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CCTTTGGGGTCCAGGCACTCAAGCTCAAGCCCACTTTGGGGGCACTACATA 60
DB 262 CCTTTGGGGTCCAGGCACTCAAGCTCAAGCCCACTTTGGGGGCACTACATA 321
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DB 322 GCCATGATCCCTCAAGTCTCTGGGGGATCTGGGCTTTGCTGCAACACAGAGGC 381
QY 121 ATCTCAGCAGCAGGCGCACTCTCACCACCCGAGAGAGACCGAGAGAGAGAGGC 180
DB 382 ATCTCAGCAGCAGGCGCACTCTCACCACCCGAGAGAGACCGAGAGAGAGAGGC 441
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DB 562 GAGTCTGAGCCCTGAGACCGCTAGAACGAGTCTCTCACTCCCGCGCTGAGAGAC 621
QY 361 CTTTGGCCGAGAGACCCAGGCCCCAGAAAAACCTTGGGCTCTTGGCCCTGAGGTGAC 420
DB 622 CTTTGGCCGAGAGACCCAGGCCCCAGAAAAACCTTGGGCTCTTGGCCCTGAGGTGAC 681

QY 421 AACGACCTCAGAGAGAGCCAGACTAGACCCCGGGAGAGATACAGATATGAGT 480
DB 682 AACGACCTCAGAGAGAGCCAGACTAGACCCCGGGAGAGATACAGATATGAGT 741
QY 481 CCCTCAGCGGTTTGTTCACAGGATCTCAGGACCCAGGCGCTCTCACCTTGAT 540
DB 742 CCCTCAGCGGTTTGTTCACAGGATCTCAGGACCCAGGCGCTCTCACCTTGAT 801
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QY 601 TTATATCGAACCCGTAAGGTGTGTCTCAATATTTCTGCTCCCTCTGAGATCGATA 660
DB 862 TTATATCGAACCCGTAAGGTGTGTCTCAATATTTCTGCTCCCTCTGAGATCGATA 921
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DB 1042 CAGGCTATGTAAGTGTGTCTCTTCTGCACTGTGTGCGCGCGAGAACTATCAGT 1101
QY 841 AGACAGCTGCTGCTTCCATGAAACGAAAAATTAATCATGTTTCTTAA 891
DB 1102 AGACAGCTGCTGCTTCCATGAAACGAAAAATTAATCATGTTTCTTAA 1152
RESULT 4
AX406002 1473 bp DNA linear PAT 14-JUN-2002
LOCUS
DEFINITION Sequence 417 from Patent WO0222660.
ACCESSION AX406002
VERSION AX406002.1 GI:21439443
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens (human)
Mammalia; Euteleostomi; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1
Tang,Y.T., Liu,C., Zhou,P., Asundi,V., Zhang,J., Zhao,Q.A., Ren,F.,
Xue,A.J., Yang,Y., Wehrman,T. and Drmanac,R.T.
Novel nucleic acids and polypeptides
Patent: WO 0222660-A 417 21-MAR-2002;
HSEQ, INC. (US)
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Best Local Similarity 99.9%; Pred. No. 0;
Matches 878; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 13 CCAGGCAACCAAGCTCAGGCTCAAGCTTTGGGGGCGAGTACATAGCATGATCTTC 72
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QY	133	GAGGGCCA CCCCCTCTCA CCGCAGAGGACCGAGAGGAGGAGCTCCCA CATTG	192
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QY	193	CCTAAGGGCCCCCAGTCCCGGGTGA CCGTTTGGCCAGGGGGACCCCGCTCTTTGAAGAT	252
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Db	885	CCTGAACCGCTGAAAGGATCTCTCA CCTCCCGGCTGACGACCTTTGGCCGCA	944
QY	373	GGACCCCA GCGCCAGAAACCCCTGGCTCTGCCCCCTGAGGTGACAACCGA CTTGAG	432
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QY	433	GAGGAGCCAGA CTTAGACCCCA CCGGAGAGTACAGATATGAGTCCCTCAGCCGT	492
Db	1005	GAGGAGCCAGA CTTAGACCCCA CCGGAGAGTACAGATATGAGTCCCTCAGCCGT	1064
QY	493	TCTGTTCCAGGACATCTCGAGGACCA GGCCTCTCCA CCGCTGTGATTCGCCGATTT	552
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QY	553	CTTCCCAATTAGCCATCTCTTAAACCTCTCTCA TCCCTCGGTTTATTCTGAAC	612
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Db	1185	CCGTAAAGTGTGTTCTCAATATTTCTGTCCCTCCTGAGATCCATA CTTAGTCTCAC	1244
QY	673	ATGCGCCGTTTTTCTCTGTGACAGCTTAAGCTACTCTCTCA CCGCTCCAGGCTCG	732
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QY	733	GGCCCA CCTACCTCCACCCGAGCTTCTGTGCGCGGCA TGTGAGGCA GGGCTATAGT	792
Db	1305	GGCCCA CCTACCTCCACCCGAGCTTCTGTGCGCGGCA TGTGAGGCA GGGCTATAGT	1364
QY	793	ACTGTGTTCCCTTCTGCACTGTGTGCGCGGAGAGAACTATCA GTAGCA GCTGTG	852
Db	1365	ACTGTGTTCCCTTCTGCACTGTGTGCGCGGAGAGAACTATCA GTAGCA GCTGTG	1424
QY	853	CTTCCATGAACGGAATAATAAATCATGTTTTCTTAA	891
Db	1425	CTTCCATGAACGGAATAATAAATCATGTTTTCTTAA	1463

RESULT 5				
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LOCUS	AB031480.	1143 bp	mRNA	linear
DEFINITION	Homo sapiens SPRI mRNA, complete cds.			PRI 08-DEC-1999
ACCESSION	AB031480			
VERSION	AB031480.1 GI:6539433			
KEYWORDS	.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
REFERENCE	1 (sites)			
AUTHORS	Oke,A., Tamiya,G., Tomizawa,M., Ota,M., Katsuyama,Y., Makino,S., Shina,T., Yoshitome,M., Lizuka,M., Saseo,Y., Iwashita,K., Kawakudo,Y., Sugai,J., Ozawa,A., Ohkido,M., Kimura,M., Bahram,S. and Inoko,H.			

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Best Local Similarity	99.9%; Pred. No. 0;
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432	CTCCCAACATTGGCTCAGAGGGCCCCCAAGTCCCGGTGACCTTTGGCCAGGGGACCCCC 491
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492	TCTCTTTGGAAGATCTCTCCGCTTACCCGCCCAAGTCGTCTCTTGGAGAACCTGTCTTAAC 551
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300	TGAGTCTGGCCCCCTGAAACGACCTTAACAGGATCTCTCAACCTCCCGGCTTGACGA 359
552	TGAGTCTGGCCCCCTGAAACGACCTTAACAGGATCTCTCAACCTCCCGGCTTGACGA 611
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360	CCCTTGGCCGACAGACCCCAAGCCCAAGAAAACCTTGGCTCTCTGCCCCCTGAGGTGA 419
612	CCCTTGGCCGACAGACCCCAAGCCCAAGAAAACCTTGGCTCTCTGCCCCCTGAGGTGA 671
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Qy 780 GCGGGCTATGTAAGTGTGTTCCCTTGCCACCTGATGCGCGGAGAGAACTATCAG 839
Db 1032 GCGGGCTATGTAAGTGTGTTCCCTTGCCACCTGATGCGCGGAGAGAACTATCAG 1091
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Db 1092 TAGACAGCTGCTGCTTCATGAAACGAAAAATATAATCATGTTTCTTAA 1143
RESULT 6
AX477396 2997 bp DNA linear PAT 12-AUG-2002
LOCUS Sequence 10 from Patent W00244375.
DEFINITION AX477396
ACCESSION AX477396
VERSION AX477396.1 GI:22216625
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1. Charmley, P., Moss, P. and Mceuen, M.
AUTHORS Compositions and methods for diagnosing or treating psoriasis
TITLE Patent: WO 0244375-A 10 06-JUN-2002;
JOURNAL Celltech R & D, Inc. (US)
FEATURES
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 775; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 117 AGGATCTCAGGCGAGGCGCCCTCTCACCACCGCAGAGAGACGAGAGGC 176
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Qy 477 GAGTCCCTCAGCGGTTCTGTTCCAGGACATCTCAAGCAGCCAGCCCTCTCACCTC 536
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LOCUS Sequence 4 from Patent W00244375.
DEFINITION AX477390
ACCESSION AX477390
VERSION AX477390.1 GI:22216619
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1. Charmley, P., Moss, P. and Mceuen, M.
AUTHORS Compositions and methods for diagnosing or treating psoriasis
TITLE Patent: WO 0244375-A 4 06-JUN-2002;
JOURNAL Celltech R & D, Inc. (US)
FEATURES
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ORIGIN
Query Match 87.0%; Score 775; DB 6; Length 3001;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 775; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 2204 AGGATCTCAGGCGAGGCGCCCTCTCACCACCGCAGAGAGACGAGAGGC 2263
Qy 177 AGGCTCCCAACATTGCTCAGGAGCCCGCAGTCCCGGTGACCTTGGCCAGGGGACCC 236
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Qy 237 CCTCTCTTGAAGATCTTCGCTTACCGCCGACGTCGTCTCTGAGAGACCTGCTGA 296
Db 2324 CCTCTCTTGAAGATCTTCGCTTACCGCCGACGTCGTCTCTGAGAGACCTGCTGA 2383
Qy 297 AACTGAGTCTGCGCCCTGTAACCGCTTGAACGAGATCTCTTAACTCCCGGCTGA 356
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QY 357 CGACCTTGGCGCGAGAGACCCAGACCCCGAGAAAACCCCTGAGCTCTGAGGT 416
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RESULT 8
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LOCUS AC004195
DEFINITION Homo sapiens clone UMGCI:Y24C027 from 6p21, complete sequence.
AC004195
VERSION AC004195.1 GI:3980474
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 40878)
AUTHORS Janer, M., Guillaudoux, T., Vu, Q., Kutyavlin, T., Harter, H. and Geraghty, D.E.
TITLE Large scale sequence analysis of the human MHC class I region
JOURNAL Unpublished (1998)
REMARK Fred Hutchinson Cancer Research Center
The Clinical Research Division
1100 Fairview Ave. N., P.O. Box 19024
Seattle, WA 98109-1024
Contact: Daniel E. Geraghty (geraghty@fhcr.org)
2 (bases 1 to 40878)
REFERENCE Geraghty, D.E. and Olson, M.V.
AUTHORS Direct Submission
TITLE Submitted (1998)
JOURNAL Submitted (23-FEB-1998) Human Genome Center, University of Washington, Box 352145, Seattle, WA 98195, USA
3 (bases 1 to 40878)
REFERENCE Geraghty, D.E. and Olson, M.V.
AUTHORS Direct Submission
TITLE Submitted (08-DEC-1998) Human Genome Center, University of Washington, Box 352145, Seattle, WA 98195, USA
JOURNAL Submitted (23-FEB-1998) Human Genome Center
Box 352145 Seattle, WA 98195
REMARK Contact: Daniel E. Geraghty (geraghty@fhcr.org)
On Dec 8, 1998 this sequence version replaced gi:2905865.
COMMENT Overlapping sequences:

5' : UMGCI:Y14C057 (Genbank Accession: AC006047)
3' : UMGCI:Y24C203

Sequence Quality Assessment:
This entry has been annotated with sequence quality estimates computed by the Phrap assembly program. All manually edited bases have been reduced to quality zero. Quality levels above 40 are expected to have less than 1 error in 10,000 bp.
Base-by-base quality values are not generally visible from the Genbank flat file format but are available as part of this entry's ASN.1 file.

Double stranded (DS) coverage: 77.6%
DS or two chemistry coverage: 100.0%
Single stranded regions: 0

Sequence Validation:
This sequence has been validated by Multiple Complete Digest Mapping. Comparison of the experimentally derived map digest fragments with sequence-predicted fragments is given below. Small fragments below a variable cutoff (approximately 400-600bp) are not mapped and hence do not appear in the table. There are no significant remaining discrepancies between the experimental and predicted values. Uniquely ordered fragment groups are separated by dashed lines.

Map BglII HindIII NotI Seq
Seq Map Seq Map Seq

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FEATURES
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 775; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

117 AGGATCTCAGGCGAGGCGACCCCTCTCACCACCGGAGAGGAGGAGGAGG 176
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27087 AGGCATCTCAGGCGAGGCGACCCCTCTCACCACCGGAGAGGAGGAGG 27146

177 AGGCTCCCAACATTCGCTCAGGCGCGCCGCTGACCCCTTGCCGAGGCGACC 236
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27147 AGGCTCCCAACATTCGCTCAGGCGCGCCGCTGACCCCTTGCCGAGGCGACC 27206

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Qy      657 CATACTATGCTCTCAATTCGCGCTTTTCTCTGACAGCTTAAGCTACTCTCTAC 716
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LOCUS
DEFINITION
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sequence.
ACCESSION
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VERSION
AL773544.5 GI:37805611
KEYWORDS
HTG.
SOURCE
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ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 113388)
AUTHORS
Almeida J.
TITL
Direct Submission
JOURNAL
Submitted (21-OCT-2003) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquerry@sanger.ac.uk Clone requests: clonerequests@sanger.ac.uk
On Oct 21, 2003 this sequence version replaced gi:22759515.

COMMENT
----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquerry@sanger.ac.uk
-----
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with

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only a small overlap as described above.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em, EMBL; SW, SWISSPROT; Tr, TREMBL; Wp, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone conigs constructed by the MHC HaploTYPE Consortium and collaborators. Further information can be found at

<http://www.sanger.ac.uk/HGP/Chr6/MHC>

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

DAOB-18511 is from a DNA-arts QBL human bac library VECTOR: pBelobAC11.

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source Location/Qualifiers

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 728; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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D 60084 AGGCTCCCAACATTTGCTTCAAGGCGCCCGCAGTCCCGGTGACCTTGGCCAGGGGACC 60025
QY 237 CCCCTCTTTGAAGATCTCTCGGCTTACCCGCCAGTCTGTCCTTGGAGAGACTGCTTGA 236
D 60024 CCCCTCTTTGAAGATCTCTCGGCTTACCCGCCAGTCTGTCCTTGGAGAGACTGCTTGA 59965
QY 297 AACTGAGTCTGAGCCCTGAAACCGCTTAAAGAGATCTCTCAACTCCCGGAGCTGA 356
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ACCESSION BD095297
VERSION BD095297.1 GI:22640885
KEYWORDS WO 0142458-A/2
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Inoko, H. and Tamaiya, G.
TITLE The method of testing for psoriasis vulgaris
JOURNAL Patent: WO 0142458-A 2 14-JUN-2001;
HIDETOSHI INOKO, GEN TAMAIYA
OS Homo sapiens (human)
PN WO 0142458-A/2
PD 14-JUN-2001
PP 06-DEC-2000 WO 2000/P008624
PR 06-DEC-1999 JP 99P 346867
PI HIDETOSHI INOKO, GEN TAMAIYA
PC C12N15/12, C12Q1/68

COMMENT

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FT exon (1282) (11405)
FT exon (1602) (11702)
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Best Local Similarity 99.9%; Pred. No. 0;
Matches 774; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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D 1873 CCCCTCTTTGAAGATCTCTCGCTTACCGCCGAGTCTGTCCTTGGAGAGACTGCTGA 1932
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ACCESSION AB088114
VERSION AB088114.1 GI:27544424
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Shihina,T., Ota,M., Katsuyama,Y., Hashimoto,N. and Inoko,H.
TITLE Genome diversity in HLA: A new strategy for detection of genetic
polymorphisms in expressed genes within the HLA class III and class
I regions
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 30911)
AUTHORS Shihina,T.
TITLE Direct Submission
JOURNAL Submitted (08-JUL-2002) Takashi Shihina, Tokai University School of
Medicine, Molecular Life Science 2; Bohseidai, Isehara, Kanagawa
259-1193, Japan (E-mail: tshihina@is.tcc.u-tokai.ac.jp,
tel:81-463-93-1121, fax:81-463-94-8884)
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 Best Local Similarity 99.9%; Pred. No. 0;
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Db 117 AGGCATCTCAGGACGCGAGGCGCCACCCCTCTCAACCCGAGAGAGAGAGAGAGG 176
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 VERSION AB023060.1 GI:5672629

KEYWORDS HTG.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (sites)
 AUTHORS Shihina,T., Tamiya,G., Oka,A., Takishima,N., Yamagata,T.,
 Kikawa,E., Iwata,K., Tomizawa,M., Okukata,N., Kuwano,Y.,
 Matanabe,K., Fukuzumi,Y., Itakura,S., Sugawara,C., Ono,A.,
 Yamazaki,M., Teshiro,H., Ando,A., Ikemura,T., Soeda,E., Kimura,M.,
 Bahram,S., and Inoko,H.
 TITLE Molecular dynamics of MHC genesis unraveled by sequence analysis of
 the 1,796,938-bp HLA class I region
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (23), 13282-13287 (1999)
 MEDLINE 20027539
 PUBMED 10557312
 REFERENCE 2 (bases 1 to 39196)
 AUTHORS Shihina,T. and Takishima,N.
 TITLE Direct Submission
 JOURNAL Submitted (29-JAN-1999) Takashi Shihina, Tokai University School of
 Medicine, Department of Molecular Life Science 2, Bohseidai,
 Isehara, Kanagawa 259-1193, Japan
 E-mail:tsuhina@is.lcc.u-tokai.ac.jp, Tel:81-463-93-1121,
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ORIGIN
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Db 117 AGGCATCTCAGGACGCGAGGCGCCACCCCTCTCAACCCGAGAGAGAGAGAGG 176
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 Qy 537 TGATTCCTCTCAAGCGCTTGTGTCTGAGAGAGAGAGAGAGAGAGG 596
 Db 11053 TGATTCCTCTCAAGCGCTTGTGTCTGAGAGAGAGAGAGAGAGAGG 11112
 Qy 597 CGGTTTATTTCTGAACCGCTGAAGGTGTGTCTCAATATTTCTGAGAGATC 656

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Db      11113 CGGTTTATTCTGAACCGTAGGAGTGTTCTCAATATTTCCGTCCCTCGAGATC 11172
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Db      11173 CATACTAGTCTCAGATTCGCGGTTTTTCTCTGACAGCTAAGCTACTCTCCACC 11232
Oy      717 TCGCTTCAGGCTCGGCGCCACCTACCTCCACCCGGTCTTCTGCGCGGCGAGTGGCT 776
Db      11233 TCGCTTCAGGCTCGGCGCCACCTACCTCCACCCGGTCTTCTGCGCGGCGAGTGGCT 11292
Oy      777 GGGGCAAGGCTAGTACTGTGTTCTCTTCTGCGCACTGGTGGCGGCGAGAACTAT 836
Db      11293 GGGGCAAGGCTAGTACTGTGTTCTCTTCTGCGCACTGGTGGCGGCGAGAACTAT 11352
Oy      837 CAGTAGACAGCTGCTGCTTCATGAAACGAAAAATATAATCATGTTTCTTAA 891
Db      11353 CAGTAGACAGCTGCTGCTTCATGAAACGAAAAATATAATCATGTTTCTTAA 11407

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RESULT 13

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AX522117 55050 bp DNA linear PAT 24-OCT-2002
LOCUS     Sequence 4 from Patent WO02064831.
DEFINITION
ACCESSION AX522117
VERSION    AX522117.1 GI:24411002
KEYWORDS
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens; Chordata; Craniata; Vertebrata; Euteleostomi;
            Eukaryota; Metazoa; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
            Leach, N.J., Allen, M.J. and Nicholson, R.K.
            Test and model for inflammatory disease
            Patent: WO 02064831-A 4 22-AUG-2002;
            Oxagen Limited (GB)
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Best Local Similarity 99.9%; Pred. No. 0;
Matches 774; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy      117 AGGCATCTCAGGCGAGGCGCACCCCTCTCAACCCGCGAGAGACCGAGAGAGGC 176
Db      27098 AGGCATCTCAGGCGAGGCGCACCCCTCTCAACCCGCGAGAGACCGAGAGAGGC 27157
Oy      177 AGGCTCCCCCAACATTGCTCTAGGGGCCCCCGAGTCCCGGTGACCTTTGGCCAGGGCAAC 236
Db      27158 AGGCTCCCCCAACATTGCTCTAGGGGCCCCCGAGTCCCGGTGACCTTTGGCCAGGGCAAC 27217
Oy      237 CCCTCTTTGAAGATCTCGGCTACCGCGCCGAGTCCCTCGAGAGACCTGGCTGA 296
Db      27218 CCCTCTTTGAAGATCTCGGCTACCGCGCCGAGTCCCTCGAGAGACCTGGCTGA 27277
Oy      297 AACTGAGTGTGGCCCCCTGAAACCGCTAGAACGAGATCTCTCAACCTCCCGGCTGA 356
Db      27278 AACTGAGTGTGGCCCCCTGAAACCGCTAGAACGAGATCTCTCAACCTCCCGGCTGA 27337
Oy      357 CGACCCCTGGCGCGAGAGACCGCCCAAAAAACCCCTGGCTCTCTCCCTCTGAGGT 416
Db      27338 CGACCCCTGGCGCGAGAGACCGCCCAAAAAACCCCTGGCTCTCTCCCTCTGAGGT 27397
Oy      417 GGAACAACGAGCTCAGAGAGAGACGAGACTAGACCAACCGCGGAGAGATACGATATG 476
Db      27398 GGAACAACGAGCTCAGAGAGAGACGAGACTAGACCAACCGCGGAGAGATACGATATG 27457
Oy      477 GAGTCCCTCAGCCGCTTCTGTTCCCAAGGACATCTCAGGCAACCAAGCCCTCTCCACCCCTC 536

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Db      27458 GAGTCCCTCAGCCGTTCTGTTCCCAAGGACATCTCAGGCAACCAAGCCCTCTCCACCCCTC 27517
Oy      537 TGATTCGCGGATTTCTTCCCAATTAGCTATTCCTTAAACCTCTCTCATTCCT 596
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Oy      597 CGGTTTATTCTGAACCGGTAGGTGTTCTCAATATTTCTGTCCCTCTGAGATC 656
Db      27578 CGGTTTATTCTGAACCGGTAGGTGTTCTCAATATTTCTGTCCCTCTGAGATC 27637
Oy      657 CATACTAGTCTCAGATTCGCGGTTTTTCTCTGACAGCTAAGCTACTCTCCACC 716
Db      27638 CATACTAGTCTCAGATTCGCGGTTTTTCTCTGACAGCTAAGCTACTCTCCACC 27697
Oy      717 TCGCTTCAGGCTCGGCGCCACCTACCTCCACCCGGTCTTCTGCGCGGCGAGTGGCT 776
Db      27698 TCGCTTCAGGCTCGGCGCCACCTACCTCCACCCGGTCTTCTGCGCGGCGAGTGGCT 27757
Oy      777 GGGGCAAGGCTAGTACTGTGTTCTCTTCTGCGCACTGGTGGCGGCGAGAACTAT 836
Db      27758 GGGGCAAGGCTAGTACTGTGTTCTCTTCTGCGCACTGGTGGCGGCGAGAACTAT 27817
Oy      837 CAGTAGACAGCTGCTGCTTCATGAAACGAAAAATATAATCATGTTTCTTAA 891
Db      27818 CAGTAGACAGCTGCTGCTTCATGAAACGAAAAATATAATCATGTTTCTTAA 27872

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RESULT 14

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AL662867/c 70288 bp DNA linear PRI 24-APR-2002
LOCUS     Human DNA sequence from clone Xkbac-34D1 on chromosome 6, complete
DEFINITION
ACCESSION AL662867
VERSION    AL662867.5 GI:20068664
KEYWORDS   HTG.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens; Chordata; Craniata; Vertebrata; Euteleostomi;
            Eukaryota; Metazoa; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
            Sycamore, N.
            Direct Submission
            Submitted (23-APR-2002) Wellcome Trust Sanger Institute, Hinxton,
            Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
            humquerry@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
            On Apr 7, 2002 this sequence version replaced gi:19309560.
            During sequence assembly data is compared from overlapping clones.
            Where differences are found these are annotated as variations
            together with a note of the overlapping clone name. Note that the
            variation annotation may not be found in the sequence submission
            corresponding to the overlapping clone, as we submit sequences with
            only a small overlap as described above.
            This sequence was finished as follows unless otherwise noted: all
            regions were either double-stranded or sequenced with an alternate
            chemistry or covered by high quality data (i.e., phred quality >=
            30); an attempt was made to resolve all sequencing problems, such
            as compressions and repeats; all regions were covered by at least
            one plasmid subclone or more than one M13 subclone; and the
            assembly was confirmed by restriction digest. The following
            abbreviations are used to associate primary accession numbers given
            in the feature table with their source databases: Em; EMBL; SW;
            SWISSPROT; Tr; TREMBL; Wp; WORMPEP; information on the WORMPEP
            database can be found at
            http://www.sanger.ac.uk/projects/C_elegans/wormpep Xkbac-34D1 is
            from a CHORI-502 human bac - COX cell line library VECTOR:
            pYARBAC2.1

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FEATURES

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/organism="Homo sapiens"

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      PTNDNSYRGLNBSQPGQSSSSSQTSVSSGQSVSSNORPCSDIDPSGSGPITS
      HSGPYLPSHSSVSGGQRPVVVVVDQHSQAGPVQGPCCNGGLPKRCPPIISVDKS
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      /number=1
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Best Local Similarity 99.9%; Pred. No. 0;
Matches 774; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  117 AGGCATCTCAGGCGAGGCGACCCCTCTCACCACCCGAGAGGACGAGAGAGGC 176
    |||||||
DB  3768 AGGCATCTCAGGCGAGGCGACCCCTCTCACCACCCGAGAGGACGAGAGAGGC 3827

QY  177 AGGCTCCCAACATTGCTCAGGCGCCGCCAGTCCCGGTGACCTTGCCAGGGGCAACC 236
    |||||||
DB  3828 AGGCTCCCAACATTGCTCAGGCGCCGCCAGTCCCGGTGACCTTGCCAGGGGCAACC 3887

QY  237 CCCTCTCTTTGAAGATCTCTCCGCTACCCGCCCAAGTGTCTCTGAGAGACTGCTCTGA 296
    |||||||
DB  3888 CCCTCTCTTTGAAGATCTCTCCGCTACCCGCCCAAGTGTCTCTGAGAGACTGCTCTGA 3947

QY  297 AACCTGAGTCTGAGCCCTCTGAACCGCCTAGAAAGGATCTCTCAACCTCCCGGCTCTGA 356
    |||||||
DB  3948 AACCTGAGTCTGAGCCCTCTGAACCGCCTAGAAAGGATCTCTCAACCTCCCGGCTCTGA 4007

QY  357 CGACCTTTGCGCGGACGAGACCCGAGCCCGAGAAAACCCCTGAGCTCTGCTCTGAGGT 416
    |||||||
DB  4008 CGACCTTTGCGCGGACGAGACCCGAGCCCGAGAAAACCCCTGAGCTCTGCTCTGAGGT 4067

QY  417 GGAACAACCGACTTCAAGAGAGCCAGACTTGAACCCCAACCCCGGAGAGATACAGATTAATG 476
    |||||||
DB  4068 GGAACAACCGACTTCAAGAGAGCCAGACTTGAACCCCAACCCCGGAGAGATACAGATTAATG 4127

QY  477 GAGTCCCTCAGCGGTTCTGTTCACAGGCAATCTCCAGGCAACCAAGCCCTCTCAACCTC 536
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DB  4128 GAGTCCCTCAGCGGTTCTGTTCACAGGCAATCTCCAGGCAACCAAGCCCTCTCAACCTC 4187
QY  537 TGAATCCCGGTGAATCTTCCCAATTTAGCCCTATCTCCCTTAAACCTTCTCATTCCTT 596
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DB  4188 TGAATCCCGGTGAATCTTCCCAATTTAGCCCTATCTCCCTTAAACCTTCTCATTCCTT 4247
QY  597 CGGTTTATTTCTGAACCCGTAAGGTGTGTTCTCAATATTTCCGTCCCTCTGAGATC 656
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DB  4248 CGGTTTATTTCTGAACCCGTAAGGTGTGTTCTCAATATTTCCGTCCCTCTGAGATC 4307
QY  657 CATACTTAGTCTCAATGCGCCGTTTCTCTGACAGCTTAAGCTTAAGCTTAAGCTTAAG 716
    |||||||
DB  4308 CATACTTAGTCTCAATGCGCCGTTTCTCTGACAGCTTAAGCTTAAGCTTAAGCTTAAG 4367
QY  717 TCGCTTCAGAGCTCGGCCCCCACTACCTCCACCCGGTCTTCTGCGCGGAGATCGCT 776
    |||||||
DB  4368 TCGCTTCAGAGCTCGGCCCCCACTACCTCCACCCGGTCTTCTGCGCGGAGATCGCT 4427
QY  777 GGGGCAAGGCTATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAAT 836
    |||||||
DB  4428 GGGGCAAGGCTATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAAT 4487
QY  837 CAGTAGACAGCTGCTGCTTTCATGAACCGAAAAATTAATATCATGTTTCTTAA 891
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DB  4488 CAGTAGACAGCTGCTGCTTTCATGAACCGAAAAATTAATATCATGTTTCTTAA 4542
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Job time : 4031 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 11, 2005, 07:08:44 ; Search time 540 Seconds
(without alignments)
8661.545 Million cell updates/sec

Title: US-09-994-365-1

Perfect score: 891

Sequence: 1 ccctctggggctccagca.....taaaatcatgtttcttaa 891

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Searched: 4134886 seqs, 2624710521 residues

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Minimum DB seq length: 0

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	891	100.0	891	6	ABK86962 Human can
2	828	92.9	1473	6	ABN60006 Novel hum
3	775	87.0	2997	6	ABK86967 Human CAN
4	775	87.0	3001	6	ABK86963 Human can
5	724	81.3	25235	4	AAH45310 Human SEE
6	724	81.3	55050	6	ABQ75680 Human SEE
7	554	62.2	565	12	ACH72505 Human gen
8	157	17.6	157	12	ACH86315 Human gen
9	60	6.7	60	6	ABN33229 Human spl
10	50	5.6	50	6	ABZ00541 Human leu
11	26	2.9	204	3	AAAC23697 Human sec
12	21	2.4	21	6	ABK86968 PCR prime
13	21	2.4	1315	10	ADBS8427 Toxicity-
14	20	2.2	229	2	AAV13900 Fragments
15	20	2.2	289	3	AAAC72265 Single nu
16	20	2.2	289	3	AAAC72286 Single nu
17	20	2.2	331	8	ABX38775 Bovine ES
18	20	2.2	395	8	ABX40716 Bovine ES
19	20	2.2	411	8	ABX39498 Bovine ES
20	20	2.2	468	4	AAK89219 Human dig
21	20	2.2	531	9	ACH38340 Human end

22	20	2.2	692	4	AA826250
23	20	2.2	692	8	ABX73591
24	20	2.2	1740	11	AD131784
25	20	2.2	1907	2	AAQ91520
26	20	2.2	2034	2	AAQ24674
27	20	2.2	2039	5	AA877988
28	20	2.2	2167	10	ADA52577
29	20	2.2	3646	12	ADP10349
30	20	2.2	3721	5	AA884395
31	20	2.2	3946	6	AA819505
32	19	2.1	19	6	ABK86969
33	19	2.1	385	4	AA839185
34	19	2.1	417	5	AA867346
35	19	2.1	458	4	AA132897
36	19	2.1	458	4	AAK26999
37	19	2.1	458	4	AAK01554
38	19	2.1	458	4	AB826585
39	19	2.1	458	5	AA101530
40	19	2.1	471	3	AAAC49645
41	19	2.1	594	6	ABK53634
42	19	2.1	688	3	AAAC49978
43	19	2.1	770	12	AD113268
44	19	2.1	964	4	AAK70006
45	19	2.1	964	4	AAK85701

ALIGNMENTS

RESULT 1	
ID	ABK86962 standard; cDNA; 891 BP.
XX	ABK86962;
XX	24-SEP-2002 (first entry)
DE	Human candidate coding sequence-1 (CAN-1) cDNA.
XX	Human; antipsoriatic; chromosome 6; candidate coding sequence-1; CAN-1;
KW	SEBK-1; STG; human leukocyte antigen C; HLA C; HLA Cw6; psoriasis; skin;
KW	keratinocyte; chronic inflammatory dermatosis; erythroderma; seborrheic;
KW	gutate; pustular variant; Reiter's disease; hyperproliferation;
KW	epidermis; differentiation; diagnosis; gene therapy; gene; ss; SN;
XX	single nucleotide polymorphism.
OS	Homo sapiens.
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FT	CDS
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FT	mat_peptide
FT	130..471
FT	/*tag= c
FT	/note= "Mature CAN-1"
FT	replac= (311,C)
FT	/*tag= d
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XX	WO20024375-A2.
XX	
XX	06-JUN-2002.
XX	
XX	27-NOV-2001; 2001MO-US044506.
XX	
XX	28-NOV-2000; 2000US-0253592P.
PR	15-DEC-2000; 2000US-0256839P.
XX	
PA	(CELL-) CELITECH R & D INC.
XX	
PI	Charmley P, Moss P, Mceuen M;

XX WPI: 2002-508513/54.
DR P-PSDB; AAU79579.
XX
PT Novel isolated CAN-1 polypeptide involved in keratinocyte proliferation
PT and differentiation, and polynucleotides encoding the polypeptide, useful
PT for diagnosing or predicting susceptibility to psoriasis in individual.
XX
PS Claim 8; Page 80-81; 95pp; English.

CC The invention discloses isolated candidate coding sequence-1 (CAN-1),
CC SEBK-1 (not defined) and STG (not defined) polypeptides, and the
CC polynucleotides encoding them. All three genes were identified due to
CC their proximity to the human leukocyte antigen C (HLA C) locus on
CC chromosome 6. The HLA Cw6 allele is associated with psoriasis and as the
CC three genes are expressed in normal skin and/or keratinocyte tissue, they
CC may also have a role in psoriasis. Psoriasis is a chronic inflammatory
CC dermatosis that is characterised by hyperproliferation of epidermal
CC cells. Possible treatments against psoriasis involve the inhibition of
CC movement of cells into the epidermis, or the inhibition of
CC hyperproliferation or abnormal differentiation of keratinocytes, by the
CC inhibition of the CAN-1, STG or SEBK-1 polypeptides binding to their
CC binding partners. The polypeptides are useful for diagnosing or
CC predicting the susceptibility to psoriasis in an individual, for
CC ameliorating the symptoms and/or progression of psoriasis and for
CC identifying agents useful for treating psoriasis or modulating the
CC activity of the polypeptide. The polypeptides are also useful for
CC enhancing the level of CAN-1, STG or SEBK-1 biological activity in a cell
CC or tissue. The nucleic acid molecules are useful as hybridisation probes
CC in diagnostic procedures (such as diagnosing the presence of psoriasis or
CC the propensity to develop psoriasis) and for suppressing the expression
CC of CAN-1 or STG gene (e.g. antisense inhibition, gene therapy).
CC Antibodies, raised against the polypeptides, are useful for decreasing
CC the level of CAN-1, STG or SEBK-1 biological activity in a cell. The
CC sequence presented is the human candidate coding sequence-1 (CAN-1) cDNA
XX
SQ Sequence 891 BP, 169 A; 339 C; 196 G; 187 T; 0 U; 0 Other;

Query Match 100.0%; Score 891; DB 6; Length 891;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 891; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTCTGGGGTTCACAGGACCCAGACTGAGCCACCCAGCTTTGGGGCCAGTACATA 60
DB 1 CCTCTGGGGTTCACAGGACCCAGACTGAGCCACCCAGCTTTGGGGCCAGTACATA 60
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QY 121 ATCTCAGGACGAGGAGCCCTCTCACCACCCGACAGAGACGAGAGGAGGC 180
DB 121 ATCTCAGGACGAGGAGCCCTCTCACCACCCGACAGAGACGAGAGGAGGC 180
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DB 181 TCCCAACATTTGCTCAGGGCCCCCAGTCCCGGTGACCTTTGGCCAGGGGCAACCCCT 240
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DB 241 CTCTTGAAGATCTCCGCTACCCGCGGAGTCTCCCTGGAGAGACCTGGCTGAACCT 300
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DB 301 GAGAGTGGCCCCCTAGAACCGCTAGAACGATCTCTCAACCTCCCGGCTGACGAC 360
QY 361 CCTTGGCCGAGACCCCGCCCAAGAAACCTCTGAGCTCTGAGGTGAGC 420
DB 361 CCTTGGCCGAGACCCCGCCCAAGAAACCTCTGAGCTCTGAGGTGAGC 420
QY 421 AACCGACTCAGAGAGCCAGACTAGACCCACCCGGGAAAGTACATATGAGCT 480
DB 421 AACCGACTCAGAGAGCCAGACTAGACCCACCCGGGAAAGTACATATGAGCT 480

QY 481 CCCCTAGCCGTTCTGTTCACAGGACCTCAGGACCCAGGCCCTCTCACCCTGTGAT 540
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DB 721 CTCAGGCTTCGAGCCCACTTACCTCCACCCGCTTCTCTGCGCGGAGTGGTGGG 780
QY 781 CAGGCTATGATCTGTGTTCTCTTCTGCACTGCTGCGCGGAGGAGAACTATCACT 840
DB 781 CAGGCTATGATCTGTGTTCTCTTCTGCACTGCTGCGCGGAGGAGAACTATCACT 840
QY 841 AGACAGCTGCTGCTTCATGAAACGAAATAATTAATCATGTTTCTTAA 891
DB 841 AGACAGCTGCTGCTTCATGAAACGAAATAATTAATCATGTTTCTTAA 891

RESULT 2
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ID AEN60006 standard; cDNA, 1473 BP.
XX
AC AEN60006;

XX 28-JUN-2002 (first entry)
XX
DE Novel human coding sequence SEQ ID NO: 417.
XX

XX Homo sapiens.
XX
PN WO200222660-A2.
XX
PD 21-MAR-2002.
XX
PF 10-SEP-2001; 2001WO-US026015.
XX
PR 11-SEP-2000; 2000US-00659671.
XX

XX (HYSE-) HYSEQ INC.
XX

PI Tang YT, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA, Ren F;
PI Xue AJ, Yang Y, Wehrman T, Drmanac RT;
XX
DR P-PSDB; ABB97593.
XX
PT An isolated polynucleotide for treating diseases associated with its
PT encoded polypeptide such as cancer and multiple sclerosis.
XX

XX Claim 1; SEQ ID NO 417; 509pp; English.
XX

XX The present invention provides the protein and coding sequences of 444
XX novel human proteins. These were isolated from expressed sequences tags
XX (ESTs). They can be used to stimulate cell growth, to regulate
XX haematopoiesis e.g. to treat aplastic anaemia, to help tissue regrowth
XX e.g. in burn treatment, to regulate the immune system e.g. to treat

multiple sclerosis, to regulate activin or inhibit e.g. to treat
CC infertility, to regulate haemostasis or thrombolysis e.g. to treat stroke
CC and cancer, to screen for drugs, to treat inflammatory conditions e.g.
CC rheumatoid arthritis, and to treat nervous system disorders e.g.
CC Parkinson's disease. The present sequence is a coding sequence of the
CC invention

XX Sequence 1473 BP; 294 A; 491 C; 382 G; 306 T; 0 U; 0 Other;

Query Match 92.9%; Score 828; DB 6; Length 1473;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 878; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 585 CCCAGGACCCAGCATGAGCCACCCAGCTTTGGGGCCAGTACATAGCATATGCTTC 644
QY 73 AACTGGAAGCTCTGGGGATCTGTGTCCTTTGCTGCAACACAGAGGCATCTCAGCAGC 132
Db 645 AACTGGAAGCTCTGGGGATCTGTGTCCTTTGCTGCAACACAGAGGCATCTCAGCAGC 704
QY 133 GAGGGCCACCCCTCTCAACCCCGCAGAGGACCGAAGAGGAGGAGGCTCCCAACTTG 192
Db 705 GAGGGCCACCCCTCTCAACCCCGCAGAGGACCGAAGAGGAGGAGGCTCCCAACTTG 764
QY 193 CCTCAGGGCCCCCAGTCCCGGAGTCCCTTTGGCAGAGGAGCCCTCTCTTTGAAGAT 252
Db 765 CCTCAGGGCCCCCAGTCCCGGAGTCCCTTTGGCAGAGGAGCCCTCTCTTTGAAGAT 824
QY 253 CCTCCGCGTACCCGCGCCAGTCTGCTCTGAGAGAGACTGCTGAATGAGTCTGGCCC 312
Db 825 CCTCCGCGTACCCGCGCCAGTCTGCTCTGAGAGAGACTGCTGAATGAGTCTGGCCC 884
QY 313 CCTGAACCGCTGAGAGAGATCTCTCAACCTCCCGGCTGACGACCTTTGGCCGCA 372
Db 885 CCTGAACCGCTGAGAGAGATCTCTCAACCTCCCGGCTGACGACCTTTGGCCGCA 944
QY 373 GGAACCCAGCCCCAGAAAAACCCCTGGGCTCTGCGCCCTGAGGAGCAACCCGACTCAG 432
Db 945 GGAACCCAGCCCCAGAAAAACCCCTGGGCTCTGCGCCCTGAGGAGCAACCCGACTCAG 1004
QY 433 GAGAGGACAGACCTGAGACCCACCCGGAGAGAGATAGTGAATGCCCTCAGCCGT 492
Db 1005 GAGAGGACAGACCTGAGACCCACCCGGAGAGAGATAGTGAATGCCCTCAGCCGT 1064
QY 493 TCTGTTCCAGGATCTTCAGGACCCAGCCGCTTCACCTCTGATTCGCCGTGAAT 552
Db 1065 TCTGTTCCAGGATCTTCAGGACCCAGCCGCTTCACCTCTGATTCGCCGTGAAT 1124
QY 553 CTTCGCCAATTAAGCTATCTCTTAACCTCTTCCTCAATCCCGGTTTATTTGTAAC 612
Db 1125 CTTCGCCAATTAAGCTATCTCTTAACCTCTTCCTCAATCCCGGTTTATTTGTAAC 1184
QY 613 CCGTAAGTGGTGTCTCAATATTTCTGTCCTCCCTCTGAGATCATACTTATGCTCAC 672
Db 1185 CCGTAAGTGGTGTCTCAATATTTCTGTCCTCCCTCTGAGATCATACTTATGCTCAC 1244
QY 673 ATGCGCCGTTTTTCTCTGACAGCCTTAAGCTTACTCTTACCTGCTTCAGGCTCG 732
Db 1245 ATGCGCCGTTTTTCTCTGACAGCCTTAAGCTTACTCTTACCTGCTTCAGGCTCG 1304
QY 733 GCGCCACCTACCTCCACCCGGTCTTCGTCGCGCGGAGTCTGGGGGAGGCTAAGT 792
Db 1305 GCGCCACCTACCTCCACCCGGTCTTCGTCGCGCGGAGTCTGGGGGAGGCTAAGT 1364
QY 793 ACTGTGTTCCCTTCTGACACCTGGTGGCCGGGAGAGAACTATCAGTAGACAGCTCTG 852
Db 1365 ACTGTGTTCCCTTCTGACACCTGGTGGCCGGGAGAGAACTATCAGTAGACAGCTCTG 1424
QY 853 CTTCGATGAACGGAATAATTAATCATGTTTCTTAA 891
Db 1425 CTTCGATGAACGGAATAATTAATCATGTTTCTTAA 1463
```

RESULT 3

ABK86967

ID ABK86967-standard; DNA; 2997 BP.

XX AC

XX ABK86967;

XX DT

24-SEP-2002 (first entry)

XX DE

Human CAN-1 deletion polymorphism genomic DNA.

XX XX

Human; antipsoriatic; chromosome 6; candidate coding sequence-1; CAN-1;

KW SEBK-1; STG; human leukocyte antigen C; HLA C; HLA Cw6; psoriasis; skin;

KW keratinocyte; chronic inflammatory dermatosis; erythroderma; seborrheic;

KW guttate; pustular variant; Reiter's disease; hyperproliferation;

KW epidermis; differentiation; diagnosis; gene therapy; gene; ds; SNP;

KW single nucleotide polymorphism; deletion polymorphism.

XX OS

XX Homo sapiens.

FH Key

Location/Qualifiers

replace(11..12,CCAGA)

/*tag= a

/note= "Deletion polymorphism"

replace(114,T)

/*tag= b

/standard name= "Single nucleotide polymorphism"

replace(361,A)

/*tag= c

/standard name= "Single nucleotide polymorphism"

replace(550,A)

/*tag= d

/standard name= "Single nucleotide polymorphism"

replace(966,G)

/*tag= e

/standard name= "Single nucleotide polymorphism"

replace(1096,T)

/*tag= f

/standard name= "Single nucleotide polymorphism"

replace(1196,A)

/*tag= g

/standard name= "Single nucleotide polymorphism"

replace(1390,T)

/*tag= h

/standard name= "Single nucleotide polymorphism"

1481..2557

/*tag= i

/product= "CAN-1"

1481..1535

/*tag= j

/number= 1

1536..2201

/*tag= k

/number= 1

replace(1677,A)

/*tag= l

/standard name= "Single nucleotide polymorphism"

replace(1875,T)

/*tag= m

/standard name= "Single nucleotide polymorphism"

replace(1982,A)

/*tag= n

/standard name= "Single nucleotide polymorphism"

replace(2016,C)

/*tag= o

/standard name= "Single nucleotide polymorphism"

replace(2107,G)

/*tag= p

/standard name= "Single nucleotide polymorphism"

2202..2557

/*tag= q

/number= 2

replace(2393,T)

FT variation

PT	/*tag=	t	/standard name=	"Single nucleotide polymorphism"
PT	replace(2651,G)			
FT	/*tag=	g	/standard name=	"Single nucleotide polymorphism"
PT	replace(2818,G)			
PT	/*tag=	t	/standard name=	"Single nucleotide polymorphism"
PT	replace(2871,C)			
PT	/*tag=	u	/standard name=	"Single nucleotide polymorphism"
XX	W0200244375-A2.			
PN				
PD	06-JUN-2002.			
XX				
PP	27-NOV-2001; 2001WO-US044506.			
XX				
PR	28-NOV-2000; 2000US-0253592P.			
PR	15-DEC-2000; 2000US-0256839P.			
XX				
PA	(CELL-) CELLTECH R & D INC.			
XX				
PI	Charmley P, Moss P, Mceuen M;			
XX				
DR	WPI; 2002-508513/54.			
XX				
PT	P-PSDB; AAU79579.			
PT				
XX				
SS	Novel isolated CAN-1 polypeptide involved in keratinocyte proliferation and differentiation, and polynucleotides encoding the polypeptide, useful for diagnosing or predicting susceptibility to psoriasis in individual.			
	Example 3, Page 92-93; 95pp; English.			

	CC	The invention discloses isolated candidate coding sequence-1 (CAN-1),
	CC	SEK-1 (not defined) and STG (not defined) polypeptides, and the
	CC	polynucleotides encoding them. All three genes were identified due to
	CC	their proximity to the human leukocyte antigen C (HLA C) locus on
	CC	chromosome 6. The HLA CW6 allele is associated with psoriasis and as the
	CC	three genes are expressed in normal skin and/or keratinocyte tissue, they
	CC	may also have a role in psoriasis. Psoriasis is a chronic inflammatory
	CC	dermatosis that is characterized by hyperproliferation of epidermal
	CC	cells. Possible treatments against psoriasis involve the inhibition of
	CC	movement of cells into the epidermis, or the inhibition of
	CC	hyperproliferation or abnormal differentiation of keratinocytes, by the
	CC	inhibition of the CAN-1, STG or SEK-1 polypeptides binding to their
	CC	binding partners. The polypeptides are useful for diagnosing or
	CC	predicting the susceptibility to psoriasis in an individual, for
	CC	ameliorating the symptoms and/or progression of psoriasis and for
	CC	identifying agents useful for treating psoriasis or modulating the
	CC	activity of the polypeptide. The polypeptides are also useful for
	CC	enhancing the level of CAN-1, STG or SEK-1 biological activity in a cell
	CC	or tissue. The nucleic acid molecules are useful as hybridization probes
	CC	in diagnostic procedures (such as diagnosing the presence of psoriasis or
	CC	the propensity to develop psoriasis) and for suppressing the expression
	CC	of CAN-1 or STG gene (e.g. antisense inhibition, gene therapy).
	CC	Antibodies, raised against the polypeptides, are useful for decreasing
	CC	the level of CAN-1, STG or SEK-1 biological activity in a cell. The
	CC	sequence presented is the human candidate coding sequence-1 (CAN-1)
	CC	deletion polymorphism genomic DNA
	XX	
SQ	Sequence	2997 BP; 617 A; 785 C; 913 G; 682 T; 0 U; 0 Other;
	Query Match	87.0%; Score 775; DB 6; Length 2997;
	Best Local Similarity	100.0%; Pred. NO. 0;
MATCHES	775; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
DY	117 AGGCATCCAGACGACGCGACGCCCTTCACCACCCGACAGACCCGAGAGAAGC	176
	2200 AGGATCTCAAGCAGCGAGGGCACCCCTTACCACCCGACAGACCCGAGAGAAGC	225
	177 AGGCTCCCCAACATTGGCTTCAGGGTCCCACACTCCCGGTGAACCTTGACCGAGGACAC	236

Db	2260	AGGCTCCCAACAACTTGGCTCAGGGGCCCCCAAGTCGCCGGTAGACCTTGGCCAGGGGAC	2319		
Qy	237	CCCTCTCTTTGAAGAATCTCTCGGCTTACC GGCCCAAGTGTCTCTGGAGAAGACTTGCTCTGA	296		
Db	2320	CCCCCTCTTTGAAGAATCCTCGGCTTACC GGCCCAAGTGTCTCTGGAGAAGACTTGCTCTGA	2379		
Qy	297	AACGTGAGTCTGGGCCCCCTGAACGAGCTAGAACGAGTCTCTCAACCTCCCGGAGCTGA	356		
Db	2380	AACGTGAGTCTGGGCCCCCTGAACGAGCTAGAACGAGTCTCTCAACCTCCCGGAGCTGA	2459		
Qy	357	CGACCCCTTGGCGGCAAGACCCGAGCCCCGAGAAAACCCCTGAGCTCTTGCCCTGAAGT	416		
Db	2440	CGACCCCTTGGCGGCAAGACCCGAGCCCCGAGAAAACCCCTGAGCTCTTGCCCTGAAGT	2499		
Qy	417	GGACAAACCGACTTCAAGAGAGCCAGACTTAGACCCACCCCGGGAAGATTCAGATATG	476		
Db	2500	GGACAAACCGACTTCAAGAGAGCCAGACTTAGACCCACCCCGGGAAGATTCAGATATG	2559		
Qy	477	GAGTCCCTTCAAGCCGCTGTGTCCCAAGGACTTCCAGGACCCAGGCGCTCTCAACCTC	536		
Db	2560	GAGTCCCTTCAAGCCGCTGTGTCCCAAGGACTTCCAGGACCCAGGCGCTCTCAACCTC	2619		
Qy	537	TGATTTCCCGGGAATTCCTCCAAATTAGCCTATCTCTTAAACCTCTTCTCTCAATCCCT	596		
Db	2620	TGATTTCCCGGGAATTCCTCCAAATTAGCCTATCTCTTAAACCTCTCTCTCAATCCCT	2679		
Qy	597	CGGTTTTATTCTGAACCCGTAGAGGTGGTGTCTCAATATTCTCTGTCCCTCTGAATC	656		
Db	2680	CGGTTTTATTCTGAACCCGTAGAGGTGGTGTCTCAATATTCTCTGTCCCTCTGAATC	2739		
Qy	657	CATACCTTAGTCCCAACACCGCCGTTTTTTCCTCTGAACGCTTAGGCTACTCTCCATCC	716		
Db	2740	CATACCTTAGTCCCAACACCGCCGTTTTTTCCTCTGAACGCTTAGGCTACTCTCCATCC	2799		
Qy	717	TCCGCTCCAGGCGCTCGGAGCCCACTACCTCCAGCCGCTCTCTCGCCGCGAGTGCCT	776		
Db	2800	TCCGCTCCAGGCGCTCGGAGCCCACTACCTCCAGCCGCTCTCTCGCCGCGAGTGCCT	2859		
Qy	777	GGGGCAGGGCTAGTGTACTGTGTCCCTTCTGCCACTGTGTGGCGGGGCGAGAACTAT	836		
Db	2860	GGGGCAGGGCTAGTGTACTGTGTCCCTTCTGCCACTGTGTGGCGGGGCGAGAACTAT	2919		
Qy	837	CAGTAGACAGTGTGCTCTCATGAAACGGAAAAATTAATTCATGTTTTCTTAA	891		
Db	2920	CAGTAGACAGTGTGCTCTCATGAAACGGAAAAATTAATTCATGTTTTCTTAA	2974		
RESULT 4					
ABK86963	standard; DNA; 3001 BP.				
ID	ABK86963				
AC	ABK86963;				
XX	24-SEP-2002	(first entry)			
DE	Human candidate coding sequence-1 (CAN-1) genomic DNA.				
XX	Human; antiposrotic; chromosome 6; candidate coding sequence-1; CAN-1;				
KW	SEK-1; STG; human leukocyte antigen C; HLA C; HLA Cm6; psoriasis; skin;				
KW	keratinocyte; chronic inflammatory dermatosis; erythroderma; seborrheic;				
KW	gutale; pustular variant; Reter's disease; hyperproliferation;				
KW	epidermis; differentiation; diagnosis; gene therapy; gene; ds; SNP; .				
KW	single nucleotide polymorphism; deletion polymorphism.				
XX	Homo sapiens.				
OS	Homo sapiens.				
XX	Key				
FT	variation				
FT	location/qualifiers				
FT	replace(11..16,CA)				
FT	/*tag= a				
FT	/note= "Deletion polymorphism"				
FT	replace(118,T)				
FT	/*tag= b				
FT	/standard_name= "Single nucleotide polymorphism"				

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FT      variation      replace(554,A)
FT      /*tag= c
FT      /standard_name= "Single nucleotide polymorphism"
FT      variation      replace(1100,T)
FT      /*tag= d
FT      /standard_name= "Single nucleotide polymorphism"
FT      variation      replace(1200,A)
FT      /*tag= e
FT      /standard_name= "Single nucleotide polymorphism"
FT      variation      replace(1394,T)
FT      /*tag= f
FT      /standard_name= "Single nucleotide polymorphism"
FT      CDS
FT      /*tag= g
FT      /product= "CAN-1"
FT      1485..2561
FT      exon
FT      /*tag= h
FT      /number= 1
FT      1540..2205
FT      intron
FT      /*tag= i
FT      /number= 1
FT      variation      replace(1681,A)
FT      /*tag= j
FT      /standard_name= "Single nucleotide polymorphism"
FT      variation      replace(1879,T)
FT      /*tag= k
FT      /standard_name= "Single nucleotide polymorphism"
FT      variation      replace(1986,A)
FT      /*tag= l
FT      /standard_name= "Single nucleotide polymorphism"
FT      variation      replace(2020,C)
FT      /*tag= m
FT      /standard_name= "Single nucleotide polymorphism"
FT      variation      replace(2111,G)
FT      /*tag= n
FT      /standard_name= "Single nucleotide polymorphism"
FT      exon
FT      2206..2561
FT      /*tag= o
FT      /number= 2
FT      variation      replace(2397,T)
FT      /*tag= p
FT      /standard_name= "Single nucleotide polymorphism"
FT      variation      replace(2655,G)
FT      /*tag= q
FT      /standard_name= "Single nucleotide polymorphism"
FT      variation      replace(2822,G)
FT      /*tag= r
FT      /standard_name= "Single nucleotide polymorphism"
FT      variation      replace(2875,C)
FT      /*tag= s
FT      /standard_name= "Single nucleotide polymorphism"
XX      MO200244375-A2.
XX
XX      06-JUN-2002.
XX
XX      27-NOV-2001; 2001MO-US044506.
XX
XX      28-NOV-2000; 2000US-0253592P.
XX      15-DEC-2000; 2000US-0256839P.
XX
XX      (CELL-) CELLTECH R & D INC.
XX
XX      Charmley P, Moss P, Mceuen M;
XX      WPI; 2002-508513/54.
XX      DR
XX      P-PSDB; AAU79579.
XX
XX      Novel isolated CAN-1 polypeptide involved in keratinocyte proliferation
XX      PT and differentiation, and polynucleotides encoding the polypeptide; useful
XX      PT for diagnosing or predicting susceptibility to psoriasis in individual.
XX
XX      Claim 18; Page 82-84; 95pd; English.
```

```
XX      The invention discloses isolated candidate coding sequence-1 (CAN-1),
CC      SEBK-1, (not defined) and STG (not defined) polypeptides, and the
CC      polynucleotides encoding them. All three genes were identified due to
CC      their proximity to the human leukocyte antigen C (HLA C) locus on
CC      chromosome 6. The HLA Cw6 allele is associated with psoriasis and as the
CC      three genes are expressed in normal skin and/or keratinocyte tissue, they
CC      may also have a role in psoriasis. Psoriasis is a chronic inflammatory
CC      dermatosis that is characterised by hyperproliferation of epidermal
CC      cells. Possible treatments against psoriasis involve the inhibition of
CC      movement of cells into the epidermis, or the inhibition of
CC      hyperproliferation or abnormal differentiation of keratinocytes, by the
CC      inhibition of the CAN-1, STG or SEBK-1 polypeptides binding to their
CC      binding partners. The polypeptides are useful for diagnosing or
CC      predicting the susceptibility to psoriasis in an individual, for
CC      ameliorating the symptoms and/or progression of psoriasis and for
CC      identifying agents useful for treating psoriasis or modulating the
CC      activity of the polypeptide. The polypeptides are also useful for
CC      enhancing the level of CAN-1, STG or SEBK-1 biological activity in a cell
CC      or tissue. The nucleic acid molecules are useful as hybridisation probes
CC      in diagnostic procedures (such as diagnosing the presence of psoriasis or
CC      the propensity to develop psoriasis) and for suppressing the expression
CC      of CAN-1 or STG gene (e.g., antisense inhibition, gene therapy).
CC      Antibodies, raised against the polypeptides, are useful for decreasing
CC      the level of CAN-1, STG or SEBK-1 biological activity in a cell. The
CC      sequence presented is the human candidate coding sequence-1 (CAN-1)
CC      genomic DNA
XX
SQ      Sequence 3001 BP; 619 A; 786 C; 914 G; 682 T; 0 U; 0 Other;
Query Match      87.0%; Score 775; DB 6; Length 3001;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 775; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      117 AGGCATTCAGGAGAGAGAGGAGCCACCTCTACACCCGAGAGAGAGAGAGAGAGGC 176
DB      2204 AGGCATTCAGGAGAGAGAGGAGCCACCTCTACACCCGAGAGAGAGAGAGAGGC 2263
QY      177 AGGCTCCCAACATGCTCAGAGGAGCCCGAGGAGCCCGGAGACCTTGAGCAGAGGAGC 236
DB      2264 AGGCTCCCAACATGCTCAGAGGAGCCCGAGGAGCCCGGAGACCTTGAGCAGAGGAGC 2323
QY      237 CCCTCTTTGGAAGATCTTCGCGCTACCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 296
DB      2324 CCCTCTTTGGAAGATCTTCGCGCTACCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2383
QY      297 AACTGAGTGGAGCCCGCTGAGACCGGCTGAGACGAGATCTCTCAACTCTCCCGGCTGA 356
DB      2384 AACTGAGTGGAGCCCGCTGAGACCGGCTGAGACGAGATCTCTCAACTCTCCCGGCTGA 2443
QY      357 CGAACCTTGGCGGAGAGAGCCGAGGAGCCCGAGAGAAACCCCTGGGCTCTGCGGCTGAGGT 416
DB      2444 CGAACCTTGGCGGAGAGAGCCGAGGAGCCCGAGAGAAACCCCTGGGCTCTGCGGCTGAGGT 2503
QY      417 GGAACAACGAGCTCAGAGAGAGGAGCAGAGCTGAGACCCAGCCGAGAGAGATGATATATG 476
DB      2504 GGAACAACGAGCTCAGAGAGAGGAGCAGAGCTGAGACCCAGCCGAGAGAGATGATATATG 2563
QY      477 GAGTCCCTCAGCGGTTCTGTTCCAGAGCTTCAGAGACCGACCGCCCTCTCAACCTC 536
DB      2564 GAGTCCCTCAGCGGTTCTGTTCCAGAGCTTCAGAGACCGACCGCCCTCTCAACCTC 2623
QY      537 TGATTCGCCGTGAATCTTCCCAATTAGCTATTCCTTAACCTCTTCTGATTCCTT 596
DB      2624 TGATTCGCCGTGAATCTTCCCAATTAGCTATTCCTTAACCTCTTCTGATTCCTT 2683
QY      CGGTTTATTCGAACCCGTAAGTGATGTTCTCAATATTTCTGTCCTCTCGAGATC 656
DB      2684 CGGTTTATTCGAACCCGTAAGTGATGTTCTCAATATTTCTGTCCTCTCGAGATC 2743
QY      657 CATACTTAGTCTCAATGCGCGTTTCTCTGAGACGCTTAAGCTTACTCTTACC 716
DB      2744 CATACTTAGTCTCAATGCGCGTTTCTCTGAGACGCTTAAGCTTACTCTTACC 2803
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QY 717 TCGGCTTCAGAGCTCGGCCCCACCTACCTCCACCCGGTCTTCTGCGCGGATGCT 776
DB 2804 TCGGCTTCAGAGCTCGGCCCCACCTACCTCCACCCGGTCTTCTGCGCGGATGCT 2863
QY 777 GGGGCAAGGCTATGCTGTTCCCTTCTGCACTGCTGGCGGCGAGAACTAT 836
DB 2864 GGGGCAAGGCTATGCTGTTCCCTTCTGCACTGCTGGCGGCGAGAACTAT 2923
QY 837 CAGTAGACAGCTGCTGCTCCATGAACGGAATAATTAATCATGTTTCTTAA 891
DB 2924 CAGTAGACAGCTGCTGCTCCATGAACGGAATAATTAATCATGTTTCTTAA 2978

RESULT 5
AAH45310
ID AAH45310 standard, DNA, 25235 BP.
AC AAH45310;
DT 01-OCT-2001 (first entry)
XX
DE Human SEBK1 DNA.
KM Human, MHC S; major histocompatibility complex S; vulgar psoriasis;
KM diagnosis; primer; SEBK1; HCR; a-helix coiled-coil rod homologue;
KM polymorphism; de.
XX
OS Homo sapiens.
XX
FH Key
FH exon 1..420
FT intron /+tag= a
FT intron 421..1281
FT exon /+tag= b
FT intron 1282..1405
FT exon /+tag= c
FT intron 1406..1601
FT exon /+tag= d
FT intron 1602..1702
FT exon /+tag= e
FT intron 1703..2351
FT exon /+tag= f
FT intron 2352..2364
FT exon /+tag= g
FT intron 2365..6286
FT exon /+tag= h
FT intron 6287..6509
FT exon /+tag= i
FT intron 6510..10416
FT exon /+tag= j
FT intron 10417..10493
FT exon /+tag= k
FT intron 10494..14243
FT exon /+tag= l
FT intron 14244..14407
FT exon /+tag= m
FT intron 14408..14243
FT exon /+tag= n
FT intron 25190..25235
FT exon /+tag= o
XX
PN WO200142458-A1.
XX
PD 14-JUN-2001.
XX
PF 06-DEC-2000; 2000MO-JP008624.
XX
PR 06-DEC-1999; 99JP-00346867.
XX
PA (INOK/) INOKO H.
XX
PI Inoko H, Tamiya G;

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XX WPI; 2001-381680/40.
XX
XX New primer DNA, useful for detecting vulgar psoriasis.
PT
XX
XX Claim 1, Page 46-62; 106pp; Japanese.
PS
XX
XX The invention relates to a method of diagnosing vulgar psoriasis using
CC primers based on the sequences of the human MHC S, SEBK1 and HCR genes.
CC By analysing the sequences of these genes in Japanese patients with
CC psoriasis and in normal subjects, it has been found that some of the
CC examined polymorphisms correlate significantly to the group of patients
CC with psoriasis. Vulgar psoriasis can therefore be diagnosed by analysing
CC these gene polymorphisms. The present sequence is the human SEBK1 gene
CC which was used to design primers for use in the invention
XX
SQ Sequence 25235 BP; 5967 A; 6703 C; 6487 G; 6078 T; 0 U; 0 Other;
Query Match 81.3%; Score 724; DB 4; Length 25235;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 774; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 117 AGGCACTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 176
DB 1753 AGGCACTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1812
QY 177 AGGCTCCCAACATTCCTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 236
DB 1813 AGGCTCCCAACATTCCTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1872
QY 237 CCTCTCTTGAAGATTCCTCCGCTACCCGAGTCCGCTGAGAGAGAGTCCCTGA 296
DB 1873 CCTCTCTTGAAGATTCCTCCGCTACCCGAGTCCGCTGAGAGAGAGTCCCTGA 1932
QY 297 AACTGAGTCTGGGCCCCCTGAAACCGCTGAAAGATTCCTCAACCTCCCGGCTGA 356
DB 1933 AACTGAGTCTGGGCCCCCTGAAACCGCTGAAAGATTCCTCAACCTCCCGGCTGA 1992
QY 357 CGACCTTGGCCCGGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 416
DB 1993 CGACCTTGGCCCGGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2052
QY 417 GGAACAACGAGCTCAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 476
DB 2053 GGAACAACGAGCTCAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2112
QY 477 GAGTCCCTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 536
DB 2113 GAGTCCCTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2172
QY 537 TGAATCCCGTGAATTCCTCCCAATTTAGGCTATCTCTTAAACCTTCTCTGATTCCT 596
DB 2173 TGAATCCCGTGAATTCCTCCCAATTTAGGCTATCTCTTAAACCTTCTCTGATTCCT 2232
QY 597 CGGTTTATTTGAAACCCGTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 656
DB 2233 CGGTTTATTTGAAACCCGTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2292
QY 657 CATACTAGTCCCAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 716
DB 2293 CATACTAGTCCCAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2352
QY 717 TCGGCTTCAGAGCTCGGCCCCACCTACCTCCACCCGGTCTTCTGCGCGGATGCT 776
DB 2353 TCGGCTTCAGAGCTCGGCCCCACCTACCTCCACCCGGTCTTCTGCGCGGATGCT 2412
QY 777 GGGGCAAGGCTATGCTGTTCCCTTCTGCACTGCTGGCGGCGAGAACTAT 836
DB 2413 GGGGCAAGGCTATGCTGTTCCCTTCTGCACTGCTGGCGGCGAGAACTAT 2472
QY 837 CAGTAGACAGCTGCTGCTCCATGAACGGAATAATTAATCATGTTTCTTAA 891
DB 2473 CAGTAGACAGCTGCTGCTCCATGAACGGAATAATTAATCATGTTTCTTAA 2527

```

RESULT 6
AB075680
ID AB075680 standard; DNA; 55050 BP.
XX
XX
AC AB075680;
XX
DT 11-NOV-2002 (first entry)
XX
DE Human SEEK1 consensus genomic DNA.
XX
XX Human; SEEK1; chromosome 6p21; inflammatory disease; antiinflammatory;
KM antiportatic; gene therapy; gene; ds.
XX
OS Homo sapiens.
XX
PN WO200264831-A2.
XX
PD 22-AUG-2002.
XX
PF 13-FEB-2002; 2002WO-GB000653.
XX
PR 13-FEB-2001; 2001GB-00003514.
XX
PA (OXAG-) OXAGEN LTD.
XX
PI Lench NJ, Allen MJ, Nicholls RK;
XX
DR WPI; 2002-667013/71.
XX
PT Polymorphisms in the SEEK1 gene and polynucleotides encoding the SEEK1
PT gene, for treating, diagnosing or determining susceptibility to SEEK1
PT mediated disease, e.g. inflammatory disease such as psoriasis.
XX
PS Claim 4; Fig 2; 69pp; English.
XX
CC The present invention describes a polynucleotide (I) comprising: (a) a
CC nucleic acid sequence (II) encoding the SEEK1 gene; (b) a nucleic acid
CC sequence (III) encoding a fragment of the SEEK1 gene; or (c) a nucleic
CC acid sequence (IV) that hybridizes under stringent conditions to the
CC polynucleotide of (II) or (III). (I) has antiinflammatory and
CC antipsoriatic activities and can be used in gene therapy. The alleles of
CC one or more polymorphisms in the SEEK1 gene can be used for the
CC manufacture of a medicament for the diagnosis and treatment of SEEK1
CC mediated disease. SEEK1 protein fragments are useful in diagnostic,
CC prognostic or therapeutic methods, or as research tools in drug
CC screening. Human SEEK1 is located to chromosome 6p21. The present
CC sequence represents a human SEEK1 nucleotide sequence
XX
SQ Sequence 55050 BP; 13076 A; 14198 C; 14560 G; 13197 T; 0 U; 19 Other;
Query Match 81.3%; Score 724; DB 6; Length 55050;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 774; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

DB 27338 CGACCCCTGGCCGGCAGAGACCCCAAGCCGCCAGAAAACCCCTGGCTCTCCGCCCTGAGGT 27397
QY 417 GGACAAACCGACCTCAGAGAGAGCCAGACCTAGACCCACCCCGGGAAGATACATATATG 476
DB 27398 GGAACAACCGACCTCAGAGAGAGCCAGACCTAGACCCACCCCGGGAAGATATATG 27457
QY 477 GAGTCCCTCAGAGCGATTCTGTCCAGAGCATCTCAGAGCAACCAAGCCCTCTCAACCTC 536
DB 27458 GAGTCCCTCAGAGCGATTCTGTCCAGAGCATCTCAGAGCAACCAAGCCCTCTCAACCTC 27517
QY 537 TGAATCCCGTGAATCTCTCCCAATTAGGCTATCTCTTAAACCTCTCTCATTCCT 596
DB 27518 TGAATCCCGTGAATCTCTCCCAATTAGGCTATCTCTTAAACCTCTCTCATTCCT 27577
QY 597 CGGTTTATTTCTGAACCCGTAAGGTGTCTTCAATATTTCTGTCCCTCTCTGAGATC 656
DB 27578 CGGTTTATTTCTGAACCCGTAAGGTGTCTTCAATATTTCTGTCCCTCTCTGAGATC 27637
QY 657 CATACCTAGTCCTCAAGATGAGCGGTTTCTCTGTGACAGCTAAGCTACTCTCTAC 716
DB 27638 CATACCTAGTCCTCAAGATGAGCGGTTTCTCTGTGACAGCTAAGCTACTCTCTAC 27697
QY 717 TCGCTTCAGAGCCTCGGCCCACTCACTTCCACCCGAGTCTTCTGCGCGAGATGCT 776
DB 27698 TCGCTTCAGAGCCTCGGCCCACTCACTTCCACCCGAGTCTTCTGCGCGAGATGCT 27757
QY 777 GGGGCAAGGCTATAGTACTGTGTCTCTCTGCACTGTGTGGCGGCGAGAACTAT 836
DB 27758 GGGGCAAGGCTATAGTACTGTGTCTCTCTGCACTGTGTGGCGGCGAGAACTAT 27817
QY 837 CAGTAGACAGCTGCTGCTTCCATGAAGAAACGAAAAATTAATCATGTTTCTTAA 891
DB 27818 CAGTAGACAGCTGCTGCTTCCATGAAGAAACGAAAAATTAATCATGTTTCTTAA 27872

RESULT 7
ACH72505
ID ACH72505 standard; DNA; 565 BP.
XX
XX ACH72505;
AC
XX 29-JUL-2004 (first entry)
DT
XX
DS Human genome derived single exon probe #5700.
XX
XX Human; probe; ss; gene expression; single exon probe; microarray;
KW alternative splicing event; genomic alteration.
XX
OS Homo sapiens.
XX
XX US2003194704-A1.
PN
XX 16-OCT-2003.
PD
XX 03-APR-2002; 2002US-00029386.
PF
XX 03-APR-2002; 2002US-00029386.
PR
XX 03-APR-2002; 2002US-00029386.
PA (PENN/) PENN S G.
PA (RANK/) RANK D R.
PA (HANZ/) HANZEL D K.
XX
PI Penn SG, Rank DR, Hanzel DK;
XX
XX WPI; 2004-119264/12.
DR
XX
PT New human genome-derived single exon nucleic acid probes useful for human
PT gene expression analysis, for identifying or characterizing alternative
PT splicing events, for assessing genomic alterations or as tools for
PT surveying tissues.
XX
XX Claim 15; SEQ ID NO 5700; 80pp; English.

XX The invention relates to a nucleic acid probe for measuring human gene
CC expression, comprising any of the 27,400 fully defined nucleotide
CC sequences in the specification, or their complements or fragments, and
CC encoding at least 8 amino acids of any of the 6888 amino acid sequences
CC fully defined in the specification. The probe is a single exon probe that
CC hybridises under high stringency conditions to a nucleic acid molecule
CC expressed in human cells or tissues. Also included are a spatially-
CC addressable set of single exon nucleic acid probes for measuring human
CC gene expression (comprising a plurality of single exon nucleic acid
CC probes cited above, where each of the plurality of probes is separately
CC and addressably isolatable or amplifiable from the plurality), a single
CC exon microarray for measuring human gene expression, a method of
CC measuring human gene expression, a vector comprising the single exon
CC probe cited above, an ORF-encoded peptide comprising at least 8
CC contiguous amino acids of any of the above-mentioned amino acid
CC sequences (optionally with conservative amino acid substitutions), an
CC isolated antibody that binds specifically to a peptide cited above,
CC methods of selling and/or licensing single exon probes or microarrays to
CC a customer desiring to measure gene expression, a method of providing
CC human gene expression data by subscription, and a computer-readable
CC storage medium which contains a database having a plurality of records
CC (each record including data on the expression of a single exon probe
CC cited above. The probe, methods and apparatus are useful in gene
CC expression analysis. The probes may be used as tools for surveying
CC tissues to detect the presence of expressed messages that contain their
CC specific exon, or in constructing genome-derived single exon microarrays.
CC In addition, the probes are used in identifying and characterising
CC alternative splicing events, in detecting and characterising gross
CC alterations in the genomic locus that includes their exon, in assessing
CC smaller genomic alterations, in printing the synthesis of nucleic acids,
CC or in expressing the ORF-encoded peptide. The present sequence is a human
CC single exon probe of the invention. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?docID=20030194704
XX
SQ Sequence 565 BP; 99 A; 227 C; 112 G; 127 T; 0 U; 0 Other;

Query Match 62.2%; Score 554; DB 12; Length 565;
Best Local Similarity 100.0%; Pred. No. 4,9e-262;
Matches 554; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 235 CCCCCTCTTTTGAAGATCTCGGCTTACCCGCCAGTGTCTCTGAGAGACTTGCCT 294
Db 1 CCCCCTCTTTTGAAGATCTCGGCTTACCCGCCAGTGTCTCTGAGAGACTTGCCT 60.
QY 295 GAAACTGGAATCGGCCCTGAAACGGCTTGAACGGATCTCTCAACTCCCGGCTT 354
Db 61 GAAACTGGAATCGGCCCTGAAACGGCTTGAACGGATCTCTCAACTCCCGGCTT 120
QY 355 GAGGACCTTGTGCGCGGAGAGACCCAGACCCCAAGAAAACCTTGCTCTGCCCCGAG 414
Db 121 GAGGACCTTGTGCGCGGAGAGACCCAGACCCCAAGAAAACCTTGCTCTGCCCCGAG 180
QY 415 GTGACACACGACTCTCAGAGAGAGCCAGACTTGAACCCACCCGGGAGAGTACAGATTA 474
Db 181 GTGACACACGACTCTCAGAGAGAGCCAGACTTGAACCCACCCGGGAGAGTACAGATTA 240
QY 475 TGAAGTCCCTCGTCAAGCGTCTGTTCACAGGACATCTCCAGGACCCAGCCCTTCCACCC 534
Db 241 TGAAGTCCCTCGTCAAGCGTCTGTTCACAGGACATCTCCAGGACCCAGCCCTTCCACCC 300
QY 535 TCTGATTCCTCCGTAATCTTCCCAATTAGCCTATCTCCTTAACTCTTCTTCATTC 594
Db 301 TCTGATTCCTCCGTAATCTTCCCAATTAGCCTATCTCCTTAACTCTTCTTCATTC 360
QY 595 CTGGGTTTATTTCTGAACCCGTAAGGTGGTGTCTCAATTTCTCTGCTCCCTCTGAGA 654
Db 361 CTGGGTTTATTTCTGAACCCGTAAGGTGGTGTCTCAATTTCTCTGCTCCCTCTGAGA 420
QY 655 TCCATCTTAGTCTCTACATGCGCGTTTCTTCTCTGACAGCTTAAAGCTTACTCTCTTA 714

Db 421 TCCATCTTAGTCTCTACATGCGCGTTTCTTCTCTGACAGCTTAAAGCTTACTCTCTTA 480
QY 715 CTTCGCTTCAGAGGCTTCGGGCCACCTACCTCCACCCGGTCTTCTCTGCGCGGCAATCG 774
Db 481 CTTCGCTTCAGAGGCTTCGGGCCACCTACCTCCACCCGGTCTTCTCTGCGCGGCAATCG 540
QY 775 CTGGGCGAGGGCTTA 788
Db 541 CTGGGCGAGGGCTTA 554

RESULT 8
ACH86315
ID ACH86315 standard; DNA; 157 BP.
XX
AC ACH86315;
DT 29-JUL-2004 (first entry)
XX
DE Human genome derived single exon probe #19510.
XX
KW Human; probe; ss; gene expression; single exon probe; microarray;
KW alternative splicing event; genomic alteration.
XX
OS Homo sapiens.
XX
PN US2003194704-A1.
XX 16-OCT-2003.
XX
XX 03-APR-2002; 2002US-00029386.
XX
PR 03-APR-2002; 2002US-00029386.
XX
PA (PENN/) PENN S. G.
PA (RANK/) RANK D R.
PA (HANZ/) HANZEL D K.
XX
PI Penn SG, Rank DR, Hanzel DK;
XX
XX WPI; 2004-119264/12.
XX
DR
PT New human genome-derived single exon nucleic acid probes useful for human
PT gene expression analysis, for identifying or characterizing alternative
PT splicing events, for assessing genomic alterations or as tools for
PT surveying tissues.
XX
XX
PS Claim 1; SEQ ID NO 19510; 80bp; English.
XX
XX The invention relates to a nucleic acid probe for measuring human gene
XX expression, comprising any of the 27,400 fully defined nucleotide
XX sequences in the specification, or their complements or fragments, and
XX encoding at least 8 amino acids of any of the 6888 amino acid sequences
XX fully defined in the specification. The probe is a single exon probe that
XX hybridises under high stringency conditions to a nucleic acid molecule
XX expressed in human cells or tissues. Also included are a spatially-
XX addressable set of single exon nucleic acid probes for measuring human
XX gene expression (comprising a plurality of single exon nucleic acid
XX probes cited above, where each of the plurality of probes is separately
XX and addressably isolatable or amplifiable from the plurality), a single
XX exon microarray for measuring human gene expression, a method of
XX measuring human gene expression, a vector comprising the single exon
XX probe cited above, an ORF-encoded peptide comprising at least 8
XX contiguous amino acids of any of the above-mentioned amino acid
XX sequences (optionally with conservative amino acid substitutions), an
XX isolated antibody that binds specifically to a peptide cited above,
XX methods of selling and/or licensing single exon probes or microarrays to
XX a customer desiring to measure gene expression, a method of providing
XX human gene expression data by subscription, and a computer-readable
XX storage medium which contains a database having a plurality of records
XX (each record including data on the expression of a single exon probe
XX cited above. The probe, methods and apparatus are useful in gene
XX expression analysis. The probes may be used as tools for surveying

CC tissues to detect the presence of expressed messages that contain their
CC specific exon, or in constructing genome-derived single exon microarrays.
CC In addition, the probes are used in identifying and characterizing
CC alternative splicing events, in detecting and characterizing gross
CC alterations in the genomic locus that includes their exon, in assessing
CC smaller genomic alterations, in priming the synthesis of nucleic acids,
CC or in expressing the ORF-encoded peptide. The present sequence is a human
CC single exon probe of the invention. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?docID=20030194704
CC
XX Sequence 157 BP; 38 A; 64 C; 38 G; 17 T; 0 U; 0 Other;
SQ
Query Match 17.6%; Score 157; DB 12; Length 157;
Best Local Similarity 100.0%; Pred. No. 1.1e-66; Indels 0; Gaps 0;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 318 ACCGCTAGAACGATCTCTCAACCTCCCGGCTGACGACCTTTGGCGGACAGACC 377
DB 1 ACCGCTAGAACGATCTCTCTCAACCTCCCGGCTGACGACCTTTGGCGGACAGACC 60
QY 378 CCAGCCCCCGAGAAAACCCCTGGCTCTCTGCTGCTGAGTGAGACCACTTCAAGAGGA 437
DB 61 CCAGCCCCCGAGAAAACCCCTGGCTCTCTGCTGCTGAGTGAGACCACTTCAAGAGGA 120
QY 438 GCCAGACTAGACCAACCCCGGAGAGTACAGATA 474
DB 121 GCCAGACTAGACCAACCCCGGAGAGTACAGATA 157

RESULT 9
ABN32329
ID ABN32329 standard; DNA; 60 BP.
AC ABN32329,
XX
DT 15-JUL-2002 (first entry)
XX
DE Human spliced transcript detection oligonucleotide SEQ ID NO:5077.
XX
KW Human; mouse; rat; splice transcript; detection; RNA transcript;
XX splice variant; transcriptome; oligonucleotide library; ss.
XX
OS Homo sapiens.
XX
PN WO200210449-A2.
XX
PD 07-FEB-2002.
XX
PF 20-JUL-2001; 2001WO-IB001903.
XX
PR 28-JUL-2000; 2000US-0221607P.
XX
PR 02-MAY-2001; 2001US-0287724P.
XX
PA (COMP-) COMPUGEN INC.
XX
PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;
XX
PI WPI; 2002-257363/30.
XX
DR
XX
PT New oligonucleotide libraries comprising oligonucleotides which
XX selectively hybridize to mRNAs transcribed from a transcription unit of a
XX genome, useful for detecting tissue-, pathology-, and developmental-
XX specific genes.
XX
PS Example 1; SEQ ID NO 5077; 47bp; English.
XX
CC The present invention describes oligonucleotide libraries for detecting
XX messenger RNAs that populate a (sub-)transcriptome, where the (sub-
XX)transcriptome comprises messenger RNAs transcribed from multiple
XX transcription units that populate a genome. The library comprises several
XX oligonucleotides, each capable of hybridizing selectively to a set of

CC messenger RNAs transcribed from a given transcription unit of the genome,
CC which encodes one or more messenger RNA splice variants. The
CC oligonucleotide libraries are useful for detecting mRNAs from a
CC biological sample, in expression profiling studies, in qualitatively or
CC quantitatively characterizing the corresponding transcriptome, and in
CC detecting RNA transcripts and splice variants of human or animal
CC transcriptomes. The libraries may also be used as specialized mini
CC libraries to detect transcripts of a sub-transcriptome under a particular
CC biological or pathological state, and so allowing the detection of tissue
CC - and pathology-specific genes such as those genes only expressed in
CC specific tissue under a specific pathological condition; to detect
CC developmental specific genes; and to detect RNA transcripts and splice
CC variants of a transcriptome of a patient suffering from a particular
CC disorder. ABN27253 to ABN59589 represent oligonucleotide sequences from
CC rats, humans and mice, which are used in the exemplification of the
CC present invention. N.B. The sequence data for this patent did not form
CC part of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.int/pub/published_pct_sequences
CC
XX Sequence 60 BP; 11 A; 25 C; 5 G; 19 T; 0 U; 0 Other;
SQ
Query Match 6.7%; Score 60; DB 6; Length 60;
Best Local Similarity 100.0%; Pred. No. 6.2e-19; Indels 0; Gaps 0;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 522 GCCCTCCACACCTCTGATTCCTCCGGAATTCCTCCCAATTAGCTTAAACC 581
DB 1 GCCCTCCACACCTCTGATTCCTCCGGAATTCCTCCCAATTAGCTTAAACC 60

RESULT 10
ABZ00541
ID ABZ00541 standard; DNA; 50 BP.
AC ABZ00541,
XX
DT 09-JAN-2003 (first entry)
XX
DE Human leukocyte gene expression profiling probe SEQ ID NO 532.
XX
KW T7; leukocyte; gene expression profiling; allograft rejection;
XX atherosclerosis; congestive heart failure; systemic lupus erythematosus;
XX rheumatoid arthritis; osteoarthritis; cytomegalovirus; infection; probe;
XX ss.
XX
OS Homo sapiens.
XX
PN WO200257414-A2.
XX
PD 25-JUL-2002.
XX
PF 22-OCT-2001; 2001WO-US047856.
XX
PR 20-OCT-2000; 2000US-0241994P.
XX
PR 08-JUN-2001; 2001US-0296764P.
XX
PA (BIOC-) BIOCARDIA INC.
XX
PI Wohlgemuth J, Fry K, Matcuk G, Altman P, Prentice J, Phillips J;
XX
PI Ly N, Woodward R, Queternous T, Johnson F;
XX
DR WPI; 2002-636525/58.
XX
PT New system for leukocyte expression profiling, diagnosing a disease, or
XX monitoring (the rate of) progression of a disease, e.g. atherosclerosis
XX or congestive heart failure, comprises diagnostic oligonucleotides.
XX
PS Claim 1; Page 342; Opp; English.
XX
CC The invention relates to a system for detecting gene expression, which
XX comprises one or two isolated DNA molecules that detect expression of a
XX gene, where the gene corresponds to any of 8143 oligonucleotides
XX (ABZ00010-ABZ08152) each having 50 base pairs (bp). The system is useful

CC for leukocyte expression profiling. It is particularly useful for
CC diagnosing a disease, monitoring (rate of) progression of a disease,
CC predicting therapeutic outcome, determining prognosis for a patient,
CC predicting disease complications in an individual or monitoring response
CC to treatment in an individual. The diseases include cardiac allograft
CC rejection, kidney allograft rejection, liver allograft rejection,
CC atherosclerosis, congestive heart failure, systemic lupus erythematosus,
CC rheumatoid arthritis, osteoarthritis or cytomegalovirus infection
CC
SQ Sequence 50 BP; 15 A; 13 C; 14 G; 8 T; 0 U; 0 Other;

Query Match 5.6%; Score 50; DB 6; Length 50;
Best Local Similarity 100.0%; Pred. No. 5.2e-14;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 820 CCGGCGGACAGAACTATCTAGTACAGCTGCTCTTCATGAAACGGAAA 869
Db 1 CCGGCGGACAGAACTATCTAGTACAGCTGCTCTTCATGAAACGGAAA 50

RESULT 11
AAC23697/c
ID AAC23697 standard; cDNA; 204 BP.

XX AAC23697;
XX
XX 06-OCT-2000 (first entry)
XX
XX Human secreted protein 5' EST, SEQ ID NO: 27772.

XX Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
XX gene therapy; chromosome mapping; ss.

XX Homo sapiens.
XX
XX EP1033401-A2.

XX
XX 06-SEP-2000.

XX 21-FEB-2000; 2000EP-00200610.

XX 26-FEB-1999; 99US-0122487P.

XX (GBST) GENSET.

XX Dumas Milne Edwards J, Duclert A, Giordano J;

XX WPI; 2000-500381/45.

XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for
XX obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
XX diagnostic, forensic, gene therapy and chromosome mapping procedures.

XX Claim 1; SEQ ID NO 27772; 71pp + Sequence Listing; English.

XX The present sequence is one of a large number of 5' ESTs derived from
XX mRNAs encoding secreted proteins. No ORF has yet been conclusively
XX identified within the present sequence. The 5' ESTs were prepared from
XX total human RNAs or polyA+ RNAs derived from 30 different tissues. EST
XX sequences usually correspond mainly to the 3' untranslated region (UTR)
XX of the mRNA because they are often obtained from oligo-dT primed cDNA
XX libraries. Such ESTs are not well suited for isolating cDNA sequences
XX derived from the 5' ends of mRNAs and even in those cases where longer
XX cDNA sequences have been obtained, the full 5' UTR is rarely included. 5'
XX ESTs are derived from mRNAs with intact 5' ends and can therefore be used
XX to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in
XX diagnostic, forensic, gene therapy and chromosome mapping procedures.
XX They are used to obtain upstream regulatory sequences and to design
XX expression and secretion vectors

XX Sequence 204 BP; 55 A; 75 C; 50 G; 24 T; 0 U; 0 Other;

Query Match 2.9%; Score 26; DB 3; Length 204;

Best Local Similarity 100.0%; Pred. No. 0.032;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 744 CTCACACCGGCTCTTCCTGCGCGGC 769

Db 26 CTCACACCGGCTCTTCCTGCGCGGC 1

RESULT 12
ABK86968
ID ABK86968 standard; DNA; 21 BP.

XX ABK86968;

XX 24-SEP-2002 (first entry)

XX PCR primer, DMO 9299, used to amplify human CAN-1 cDNA.

XX Human; antipsoriatic; chromosome 6; candidate coding sequence-1; CAN-1;
XX SEBK-1; STG; human leukocyte antigen C; HLA C; HLA Cw6; psoriasis; skin;
XX keratinocyte; chronic inflammatory dermatosis; erythroderma; seboretic;
XX gutate; pustular variant; Reiter's disease; hyperproliferation;
XX epidermis; differentiation; diagnosis; gene therapy; PCR; primer; ss;
XX DMO 9299.

XX Homo sapiens.

XX MO200244375-A2.

XX 06-JUN-2002.

XX 27-NOV-2001; 2001MO-US044506.

XX 28-NOV-2000; 2000US-0253592P.

XX 15-DEC-2000; 2000US-0256839P.

XX (CELL-) CELLTECH R & D INC.

XX Charley P, Moes P, Mceuen M;

XX WPI; 2002-508513/54.

XX Novel isolated CAN-1 polypeptide involved in keratinocyte proliferation
XX and differentiation, and polynucleotides encoding the polypeptide, useful
XX for diagnosing or predicting susceptibility to psoriasis in individual.
XX Example 2; Page 44; 95pp; English.

XX The invention discloses isolated candidate coding sequence-1 (CAN-1),
XX SEBK-1 (not defined) and STG (not defined) polypeptides, and the
XX polynucleotides encoding them. All three genes were identified due to
XX their proximity to the human leukocyte antigen C (HLA C) locus on
XX chromosome 6. The HLA Cw6 allele is associated with psoriasis and as the
XX three genes are expressed in normal skin and/or keratinocyte tissue, they
XX may also have a role in psoriasis. Psoriasis is a chronic inflammatory
XX dermatosis that is characterised by hyperproliferation of epidermal
XX cells. Possible treatments against psoriasis involve the inhibition of
XX movement of cells into the epidermis, or the inhibition of
XX hyperproliferation or abnormal differentiation of keratinocytes, by the
XX inhibition of the CAN-1, STG or SEBK-1 polypeptides binding to their
XX binding partners. The polypeptides are useful for diagnosing or
XX predicting the susceptibility to psoriasis in an individual, for
XX ameliorating the symptoms and/or progression of psoriasis and for
XX identifying agents useful for treating psoriasis or modulating the
XX activity of the polypeptide. The polypeptides are also useful for
XX enhancing the level of CAN-1, STG or SEBK-1 biological activity in a cell
XX or tissue. The nucleic acid molecules are useful as hybridisation probes
XX in diagnostic procedures (such as diagnosing the presence of psoriasis or
XX the propensity to develop psoriasis) and for suppressing the expression
XX of CAN-1 or STG gene (e.g. antisense inhibition, gene therapy).
XX Antibodies, raised against the polypeptides, are useful for decreasing
XX the level of CAN-1, STG or SEBK-1 biological activity in a cell. The
XX sequence presented is the PCR primer, DMO 9299, used to amplify human

CC candidate coding sequence-1 (CAN-1) cDNA
XX Sequence 21 BP; 4 A; 10 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 2.4%; Score 21; DB 6; Length 21;
Best Local Similarity 100.0%; Pred. No. 9.9;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 GACTCAGCCGACCCAGCTTT 45
DB 1 GACTCAGCCGACCCAGCTTT 21

RESULT 13
ADB58427/c
ID ADB58427 standard; DNA; 1315 BP.

XX ADB58427;

XX 04-DEC-2003 (first entry)

XX Toxicity-related gene, SEQ ID 3453.

XX Toxic; toxin; gene expression profile; hepatotoxicity; liver;

XX drug screening; toxicity assay; ds.

XX Unidentified.

XX WO2003064624-A2.

XX 07-AUG-2003.

XX 31-JAN-2003; 2003WO-US003194.

XX 31-JAN-2002; 2002US-00060087.

XX 15-MAR-2002; 2002US-0364045P.

XX 15-MAR-2002; 2002US-0364055P.

XX 30-DEC-2002; 2002US-0436643P.

XX (GENE-) GENE LOGIC INC.

XX Mendrick D, Porter M, Johnson K, Higgs B, Caastle A, Elashoff M;

XX WPI; 2003-689530/65.

XX Predicting a toxic effect of a compound, useful in identifying toxicity

XX markers in liver tissues or cells for drug screening and toxicity assays,

XX PT comprises preparing gene expression profile of tissue or cells exposed to

XX the compound.

XX Claim 1; SEQ ID NO 3453; 1156bp; English.

XX The present invention relates to a method for predicting a toxic effect

XX of a compound. The method comprises preparing a gene expression profile

XX of a tissue or cell sample exposed to the compound, and comparing the

XX gene expression profile to a database comprising SEQ ID 1-4925, where

XX differential expression of the gene indicates at least one toxic effect.

XX The method is useful for predicting at least one toxic effect of a

XX compound, predicting hepatotoxicity or the progression of a toxic effect

XX of a compound, identifying an agent that modulates the onset or

XX progression of a toxic response, predicting the cellular pathways that a

XX compound modulates in a cell, and identifying an agent that modulates at

XX least one activity of a protein. The method and compositions of the

XX present invention using a database of genes having liver toxin-induced

XX differential expression, are useful in identifying toxicity markers in

XX liver tissues or cells for drug screening and toxicity assays. Note: The

XX sequence data for this patent did not form part of the printed

XX specification, but was obtained in electronic format directly from WIPO

XX at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 1315 BP; 251 A; 384 C; 344 G; 336 T; 0 U; 0 Other;

XX Query Match 2.4%; Score 21; DB 10; Length 1315;

Best Local Similarity 100.0%; Pred. No. 8.7;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 364 TGGCCGCGAGACCCGACCC 384
DB 210 TGGCCGCGAGACCCGACCC 190

RESULT 14
AAV13900/c
ID AAV13900 standard; DNA; 229 BP.

XX AAV13900;

XX 18-JUN-1998 (first entry)

XX Fragments of the cDNA encoding c-mpl.

XX Driver DNA sequence; subtractive amplification; amplification; RNA;

XX selective amplification; diagnosis; genetic disease; mutation;

XX thrombopoietin receptor; c-mpl; 86.

XX Unidentified.

XX WO9741260-A2.

XX 06-NOV-1997.

XX 29-APR-1997; 97WO-US007253.

XX 29-APR-1996; 96US-00639763.

XX (GENE-) GENESCAPE INC.

XX Malek LT, Sooknunan RR;

XX WPI; 1998-086521/08.

XX Subtractive amplification method - useful in the diagnosis of genetic

XX disease, mutation or variation.

XX Example 2; Page 77; 111pp; English.

XX The present sequence represents nucleotides 29 to 197 of the cDNA of

XX thrombopoietin receptor (c-mpl). It was produced using primers AAV13897-

XX 88. The present sequence was ligated into the plasmid pCAT, which is used

XX for the preparation of tester RNA sequences from c-mpl. It can be used

XX for in vitro transcription with T7 polymerase to generate RNA that can be

XX amplified using primers AAV13893-94. The method of the invention,

XX subtractive amplification, is used to preferentially amplify target RNA

XX relative to non-target RNA from a test sample of RNA. It comprises

XX contacting the sample with driver sequences complementary to the non-

XX target RNA under conditions suitable for hybridisation, extending a

XX nucleic acid primer using the target RNA as a template to form a DNA

XX template complementary to at least a portion of the target RNA, extending

XX the DNA template using an annealed promoter template to form extended

XX complementary DNA and transcribing the extended DNA template to form

XX synthetic target RNA. The method is used for the selective amplification

XX of an RNA target sequence from a mixed RNA sample. This may be applied to

XX the diagnosis of genetic disease, mutation or variation

XX Sequence 229 BP; 51 A; 69 C; 54 G; 55 T; 0 U; 0 Other;

XX Query Match 2.2%; Score 20; DB 2; Length 229;

XX Best Local Similarity 100.0%; Pred. No. 29;

XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX QY 81 GCTCCTGGGATCTGTGTC 100

XX DB 158 GCTCCTGGGATCTGTGTC 139

XX RESULT 15

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OM nucleic - nucleic search, using sw model

Run on: January 11, 2005, 09:13:15 : Search time 3418 Seconds
(without alignments)
9499.064 Million cell updates/sec

Title: US-09-994-365-1

Perfect score: 891
Sequence: 1 ccccttgggtccaccagca.....taaaatcatgtctcttaa 891

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 32822875 seqs, 18219865908 residues

Word size : 0

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

EST:
1: gb_ests1:
2: gb_ests2:
3: gb_ests3:
4: gb_ests4:
5: gb_ests5:
6: gb_ests6:
7: gb_ests7:
8: gb_ests8:
9: gb_ests9:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	305	34.2	419	2	BF513178 UI-H-BM1-
C 2	201	22.6	236	1	AI150762 qc06e04.x
C 3	174	19.5	243	8	AQ357151 CITBI-EI-
C 4	129	14.5	372	8	AQ136453 HS_3040_B
C 5	77	8.6	763	8	AF057073 AF057073
C 6	38	4.3	332	1	AA763309 vv89h03.x
C 7	38	4.3	361	1	AA168568 ms31c08.x
C 8	38	4.3	379	1	AA791103 vv91802.x
C 9	38	4.3	416	9	CG481452 OST13885
C 10	38	4.3	422	1	AI596929 vj46e11.y
C 11	38	4.3	442	9	CG487403 OST22893
C 12	38	4.3	451	1	AA798896 vv94e08.x
C 13	38	4.3	451	9	CG484009 OST17807
C 14	38	4.3	489	8	BH098389 RPCT-24-3
C 15	38	4.3	562	1	AA530301 vj46e11.x
C 16	38	4.3	669	9	CG484609 OST18617
C 17	26	2.9	332	9	CG474695 OST2738 M
C 18	26	2.9	333	2	AM315342 12593 MAR
C 19	26	2.9	395	9	CG528207 OST107284
C 20	26	2.9	655	5	BX118051 BX118051
C 21	25	2.8	283	9	CG474588 OST2539 M
C 22	25	2.8	366	9	CG474680 OST2720 M
C 23	25	2.8	415	1	AA126588 z117f08.x
C 24	25	2.8	475	9	CG473878 OST1668 M

25	2.7	593	7	CF765720	CF765720 CES001471
24	2.7	634	7	CF764947	CF764947 CES003088
27	2.6	454	7	BF902421	BF902421 CM1-MT024
26	2.6	579	8	AZ336625	AZ336625 IM0067C05
28	2.5	431	2	AM342146	AM342146 GtHEB732
C 29	2.4	480	8	AQ334387	AQ334387 HS_5001_B
C 30	2.4	519	2	AM761913	AM761913 u151d02.y
C 31	2.4	588	9	CL590154	CL590154 OB_Ba009
C 32	2.4	736	9	CL562924	CL562924 OB_Ba002
C 33	2.4	766	9	CNS04A3T	AL281378 Tetradon
C 34	2.4	899	1	AL555610	AL555610 AL555610
C 35	2.4	927	3	CR709529	CR709529 Tetradon
C 36	2.4	993	9	CNS03Q9H	AL255662 Tetradon
C 37	2.2	129	8	AZ123627	AZ123627 RPCT-23-1
C 38	2.2	302	2	BB229733	BB229733 BB229733
C 39	2.2	337	4	BI042160	BI042160 MR4-MT014
C 40	2.2	340	9	CE623904	CE623904 L3GT-988-
C 41	2.2	348	2	BB793764	BB793764 BB793764
C 42	2.2	418	2	BF057445	BF057445 7K44805.x
C 43	2.2	418	7	R80330	R80330 Y196B03.x1
C 44	2.2	437	2	AM426796	AM426796 61561 MAR
C 45	2.2	437	2	AM426796	AM426796 61561 MAR

ALIGNMENTS

RESULT 1
BF513178/c
LOCUS
DEFINITION
UI-H-BM1-am]-d-04-0-UI.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone
IMAGE:3070111 3', mRNA sequence.
BF513178
ACCESSION
BF513178
VERSION
BF513178.1 GI:11598357
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens

REFERENCE
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 419)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

AUTHORS
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)

JOURNAL
Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov

COMMENT
The sequence contained an oligo-dT track that was present in the
oligonucleotide that was used to prime the synthesis of first
strand cDNA and therefore this may represent a bonafide poly A
tail. cDNA library Preparation: M.B. Soares Lab Clone distribution:
NCI-CGAP clone distribution information can be found through the
I.M.A.G.E. Consortium/ILMIL at:
www.bio.liml.gov/db/tp/ncicgap/ncicgap.html
Seq primer: M13 Forward
POLYA=yes.

FEATURES

source

1..419
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3070111"
/lab_host="DH10B (Life Technologies)"
/clone_1ib="NCI CGAP Sub7"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; NCI_CGAP_Sub7
is a subcloned library derived from NCI_CGAP_Sub6. The
NCI CGAP Sub7 library had 12 million recombinants. A
single-stranded DNA preparation of NCI CGAP Sub6 was used
as a tracer in a subtractive hybridization with a diver
comprising: the IMAGE pool (NCI CGAP kid3 pool 1 LLM
3334-3337, 3682-3683, 3798-3803 (IMAGE Clones)
132376-132391, 145608-145675, 150052-150285);
NCI CGAP Kids pool 1 LLM 3338-3342, 3722-3725, 3776-3778
(IMAGE Clones) 1323912-1325831, 1471368-1472903,

1492104-1493255); NCI CGAP Lu5 pool 1 L1AM 3575-3582, 3851-3854 (IMAGE Clonoids 1414920-1417991, 1520904-1522439); NCI CGAP G4 pool 1 L1AM 3164-3167, 3716-3720, 3733-3735 (IMAGE Clonoids 1257096-1258631, 1469064-1470983, 1475592-1476743); NCI CGAP Pr22 pool 1 L1AM 2457-2459, 2758-2759, 3062-3068 (IMAGE Clonoids 985608-986759, 1101192-1101959, 1217928-1220615); NCI CGAP Colo pool 1 L1AM 2644-2653, 2871-2872 (IMAGE Clonoids 1057416-1061255, 1144584-1145351). (6% of the driver population), plus a pool of 3,840 arrayed clones from NCI CGAP Sub1 (IMAGE Clonoids 2708616-2710535) and NCI CGAP Sub2 (IMAGE Clonoids 2710536-27112455) (4% of the driver population), plus a pool of 11,136 clones from NCI CGAP Sub3 (IMAGE Clonoids 2712456-2723591) (10% of the driver population), plus a pool of 5,472 clones from NCI CGAP Sub4 (IMAGE Clonoids 2723592-2729326) (40% of the driver population), plus a pool of 4032 clones from NCI CGAP Sub6 (IMAGE Clonoids 2728969-2733190) (40% of the driver population). Subtraction was performed as previously described [Bonaldo, Lennon & Soares (1996) : Normalization and Subtraction: Two Approaches to Facilitate Gene Discovery. Genome Research 6, 791-806. TAG_TISSUE=ovary TAG_LIB=NCI CGAP_Ov18 TAG_SEQ=GCCACA"]

ORIGIN

Query Match 34.2%; Score 305; DB 2; Length 419;
Best Local Similarity 99.5%; Pred. No. 1.36-148;
Matches 405; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

465 GTACAGATAATGAGATCCCTCCAGCCGTTCTGTTCCAGGAGATCCAGACCCAGCC 524
419 GTACAGATAATGAGATCCCTCCAGCCGTTCTGTTCCAGGAGATCCAGACCCAGCC 360
525 CTCTCCACCCCTGATATCCCGTGAATTTCTCCAAATTTAGGCTATCTCTTAACTCT 584
359 CTCTCCACCCCTGATATCCCGTGAATTTCTCCAAATTTAGGCTATCTCTTAACTCT 300
585 TCCATATCCCTGATATCCCGTGAATTTCTCCAAATTTAGGCTATCTCTTAACTCT 644
299 TCCATATCCCTGATATCCCGTGAATTTCTCCAAATTTAGGCTATCTCTTAACTCT 240
645 CTCTCCACCCCTGATATCCCGTGAATTTCTCCAAATTTAGGCTATCTCTTAACTCT 704
239 CTCTCCACCCCTGATATCCCGTGAATTTCTCCAAATTTAGGCTATCTCTTAACTCT 180
705 TACTCTCTACCTGCTCCAGGCTCCAGGCTCCAGGCTCCAGGCTCCAGGCTCCAGGCT 764
179 TACTCTCTACCTGCTCCAGGCTCCAGGCTCCAGGCTCCAGGCTCCAGGCTCCAGGCT 120
765 CGCGCATCGCTGCGGAGGAGGCTATGTTCTGTTCCCTTCCAGGCTGAGGCGG 824
119 CGCGCATCGCTGCGGAGGAGGCTATGTTCTGTTCCCTTCCAGGCTGAGGCGG 60
825 GCGAGGAGCTATGTTCTGTTCCCTTCCAGGCTGAGGCGG 871
59 GCGAGGAGCTATGTTCTGTTCCCTTCCAGGCTGAGGCGG 13

RESULT 2

A1150762/c 336 bp mRNA linear EST 30-SEP-1998
LOCUS A1150762
DEFINITION qc0604.x1 Soares fetal heart MbH19W Homo sapiens cDNA clone
IMAGE:1708830 3', mRNA Sequence.
ACCESSION A1150762
VERSION A1150762.1 GI:3679231
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 336)
AUTHORS NCI CGAP
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Straubeberg, Ph.D.
Email: cgaaps-remail.nih.gov
This clone is available royalty-free through LML; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40ml3 fwd. RT from Amersham
High quality sequence stop: 315.
Location/Qualifiers
1. 336
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1708830"
/sex="unknown"
/dev stage="19 weeks"
/lab host="DH10B (ampicillin resistant)"
/clone lib="Soares fetal heart MbH19W"
/note="Organ: heart; Vector: pT73D (Pharmacia) with a
modified polylinker; Site 1: Not 1; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - Oligo(dT) primer [5'
TGTTCACCAATCTGAGTGGAGCGGCGGCGGATCTTTTCTTTTCTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT73 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by
M. Fatima Bonaldo. This library was constructed from the
same fetus as the fetal lung library, Soares fetal lung
MbH19W."

ORIGIN

Query Match 22.6%; Score 201; DB 1; Length 336;
Best Local Similarity 99.6%; Pred. No. 6.6e-94;
Matches 251; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

608 TGAACCCGTAAGTGTGTTCTCAATATTCCTGTCCTCCAGATCCATATTAAGC 667
285 TGAACCCGTAAGTGTGTTCTCAATATTCCTGTCCTCCAGATCCATATTAAGC 226
668 CTCAATATTCCTGTCCTCCAGATCCATATTAAGC 727
225 CTCAATATTCCTGTCCTCCAGATCCATATTAAGC 166
728 CCTGGCCCACTTACCTCCAGCCGCTTCTGCGCGGAGTGGGCAAGGCT 787
165 CCTGGCCCACTTACCTCCAGCCGCTTCTGCGCGGAGTGGGCAAGGCT 106
788 ATGTGATGTTGTTCTGTCCTGTCCTGTCCTGTCCTGTCCTGTCCTGTCCTGTCCT 847
105 AGGATGTTGTTCTGTCCTGTCCTGTCCTGTCCTGTCCTGTCCTGTCCTGTCCTGTCCT 46
848 TGTGCTTCCAT 859
45 TGTGCTTCCAT 34

RESULT 3

AQ357151/c 243 bp DNA linear GSS 24-JAN-1999
LOCUS AQ357151
DEFINITION CIRBI-EI-2534014.TF CIRBI-EI Homo sapiens genomic clone 2534014,
genomic survey sequence.
ACCESSION AQ357151
VERSION AQ357151.1 GI:4184324
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 243)

AUTHORS Zhao, S., Adams, M.D., Nierman, W., Malek, J., Shilzya, H., Simon, M. and
 Venter, J.C.
TITLE End Sequences from CalTech Libraries for Sequence-Ready
 Map Building
JOURNAL Unpublished (1997)
COMMENT Other GSSs: CITBI-EI-2534014.TR

Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
Email: hbe@cigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tcdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: M13-21
Class: BAC ends.

FEATURES	location/Qualifiers
source	1. 243
	/organism="Homo sapiens"
	/mol_type="genomic DNA"
	/db_xref="taxon:9606"
	/clone="2534014"
	/sex="male"
	/cell_type="sperm"
	/clone_1b="CITR1-E1"
	/note="Vector: pBeloBAC11; Site_1: EcoRI; Site_2: EcoRI"
	Caltech Human BAC Library D"

Query Match	174;	Score 174;	DB 8;	Length 243;
Best Local Similarity	100.0%;	Pred. No. 1e-79;		
Matches 174;	Conservative 0;	Mismatches 0;	Gaps 0;	

Qy	315	TGATACGCGCTAGAACGGAATCTCTCAACCTCCCGGCGCTAGCAACCTTGTGGCGGGAGG	374
Db	228	TGAACGCGCTAGAACGGAATCTCTCTCAACCTCCCGGCGCTAGCAACCTTGTGGCGGGAGG	169
Qy	375	ACCCGAGCCCCGAGAAACCTCTGGGCTCTGCGCCCTGAGGTGGACAACGCGACTTCAGGA	434
Db	168	ACCCGAGCCCCGAGAAACCTCTGGGCTCTGCGCCCTGAGGTGGACAACGCGACTTCAGGA	109
Qy	435	GGAGCCAGACCTTAGACCCCAACCCCGGAGAGATACAGATTAATGAGATCCCTCTAG	488
Db	108	GGAGCCAGACCTTAGACCCCAACCCCGGAGAGATACAGATTAATGAGATCCCTCTAG	55

RESULT 4	
AQ136453	
LOCUS	372 bp DNA linear GSS 24-Sep-1998
DEFINITION	HS 304.0 B2 P03 MF CTT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3040 Col=6 Row=L, genomic survey sequence.
ACCESSION	AQ136453
VERSION	AQ136453.1 GI:3527789
KEYWORDS	GSS.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens

REFERENCE	AUTHORS	TITLE	JOURNAL	MEDLINE	PUBMED	COMMENT
1 (bases 1 to 372)	Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.	Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome	Proc. Nat'l. Acad. Sci. U.S.A.	96 (17), 9739-9744 (1999)	99380589	
	Contact: Mahairas GG, Wallace JC, Hood L				10449764	
	High Throughput Sequencing Center					
	University Of Washington					

```

401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 3040 row: L column: 6
Class: BAC ends
High quality sequence strop: 372.
Location/Qualifiers
1. .372

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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="plate:3040 Col=6 Row=L"
/sex="male"
/clone_id="CIT Approved Human Genomic Sperm Library D"
/note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
E-Coli DH10B"

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	Query Match	14.5%	Score 129	DB 8	Length 372
	Best Local Similarity	99.4%	Pred. No. 5e-56		
	Matches 179	Conservative 0	Mismatches 1	Indels 0	Gaps 0
QY	684	TTTCTCTGACAGCCTAAGCCTACTCTCTCTACCTGCGCTCCAGGCGTTGCGCCACCTAC			743
Db	26	TTTCTCTGACAGCCTAAGCCTACTCTCTCTACCTGCGCTCCAGGCGTTGCGCCACCTAC			85
QY	744	CTCCACCCGGCTCTTCTGCGCCGCGCGCATGCGTGGGCGAGGGCTATGCTATGCTGCTTCC			803
Db	86	CTCCACCCGGCTCTTCTGCGCCGCGCGCATGCGTGGGCGAGGGCTATGCTATGCTGCTTCC			145
QY	804	TTTCGCAACCTGGGCGCGCGCGGAGGAACTATAGTAAAGACGGTGCCTTCATGAA			863
Db	146	TTTCGCAACCTGGGCGCGCGCGGAGGAACTATAGTAAAGCTGCTGCTTCATGAA			205

RESULT	5
AF057073/c	
LOCUS	763 bp DNA linear
DEFINITION	APF057073 Human Homo sapiens genomic clone 3R probe, GSS 21-FEB-2001 sequence.
ACCESSION	AF057073
VERSION	AF057073.1 GI:3142380
KEYWORDS	GSS.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens

REFERENCE	Eukaryotes; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
AUTHORS	1 (bases 1 to 763)
TITLE	Janer, M. and Geraghty, D. B.
JOURNAL	The human major histocompatibility complex: 42,221 bp of genomic
MEDLINE	sequence, high-density sequence-tagged site map, evolution, and
PUBMED	polymorphism for HLA class I
COMMENT	Genomics 51 (1), 35-44 (1998)
	9693031
	Contact: Janer M

Fred Hutchinson Cancer Research Center
1100 Fairview Ave., D2-100, Seattle, WA 98109-1024, USA
Email: geraghty@fhcrc.org
Class: unknown.

```

FEATURES
  source
    location/Qualifiers
      1..763
        /organism="Homo sapiens"
        /mol_type="genomic DNA"
        /db_xref="taxon:9606"
        /map="6p21.3: HLA Class I region"
        /clone="3R probe"
        /clone_lb="human"

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ORIGIN

Query Match 8.6%; Score 77; DB 8; Length 763;
 Best Local Similarity 100.0%; Pred. No. 1.2e-28;
 Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTCTTGGGGTTCCAGGACCCAGACTACGCCACCTTGGGGGCCAGTATATA 60
 DB 155 CCTCTTGGGGTTCCAGGACCCAGACTACGCCACCTTGGGGGCCAGTATATA 96

QY 61 GCCATGATCCCACTG 77
 DB 95 GCCATGATCCCACTG 79

RESULT 6
 AA763309 332 bp mRNA linear EST 27-JAN-1998
 LOCUS vW91a02.r1 Stratagene mouse skin (#937313) Mus musculus cDNA clone
 DEFINITION IMAGE:1229621 5', mRNA sequence.

ACCESSION AA763309 GI:2813056
 VERSION AA763309
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 332)
 Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Giesel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.

TITLE The WashU-HMI Mouse EST Project
 JOURNAL Unpublished (1996)
 COMMENT Contact: Marra M/Mouse EST Project
 WashU-HMI Mouse EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810

Email: mouseest@wustl.edu
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.lnl.gov) for further information.
 MGI:655213
 Seq primer: -28ml3 rev1 ET from Amersham
 High quality sequence stop: 329.

FEATURES
 source Location/Qualifiers

1.332
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6"
 /db_xref="taxon:10090"
 /clone="IMAGE:1229621"
 /sex="females"
 /tissue_type="whole skin"
 /dev_stage="11 weeks old"
 /lab_host="SOLR (kanamycin resistant)"
 /clone_1lb="Stratagene mouse skin (#937313)"
 /note="Organ: Skin; Vector: pBluescript SK-; Site 1: EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer: Oligo dt. Whole skin from 11 week old C57BL/6 female mice. Average insert size: 1.0 kb; Uni-ZAP XR Vector; ~5' adaptor sequence: 5' GAATTCGGACGAG 3' ~3' adaptor sequence: 5' CTCGAGTTTCTTTTCTTTT 3'"

ORIGIN

Query Match 4.3%; Score 38; DB 1; Length 332;
 Best Local Similarity 100.0%; Pred. No. 3.6e-08;
 Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 377 CCAGAGCCCCAGAAAACCCCTGGGCTCTGCTGAG 414
 DB 215 CCAGAGCCCCAGAAAACCCCTGGGCTCTGCTGAG 252

RESULT 7
 AA168568 361 bp mRNA linear EST 12-FEB-1997
 LOCUS m31c08.r1 Stratagene mouse skin (#937313) Mus musculus cDNA clone
 DEFINITION IMAGE:608558 5', mRNA sequence.

ACCESSION AA168568 GI:1746771
 VERSION AA168568
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 361)
 Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Giesel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.

TITLE The WashU-HMI Mouse EST Project
 JOURNAL Unpublished (1996)
 COMMENT Contact: Marra M/Mouse EST Project
 WashU-HMI Mouse EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810

Email: mouseest@wustl.edu
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.lnl.gov) for further information.
 MGI:373990
 Putative full length read
 vector to vector length is 515
 Seq primer: -28ml3 rev1 ET from Amersham
 High quality sequence stop: 352.

FEATURES
 source Location/Qualifiers

1.361
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 /strain="C57BL/6"
 /db_xref="taxon:10090"
 /clone="IMAGE:608558"
 /sex="females"
 /tissue_type="whole skin"
 /dev_stage="11 weeks old"
 /lab_host="SOLR (kanamycin resistant)"
 /clone_1lb="Stratagene mouse skin (#937313)"
 /note="Organ: Skin; Vector: pBluescript SK-; Site 1: EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer: Oligo dt. Whole skin from 11 week old C57BL/6 female mice. Average insert size: 1.0 kb; Uni-ZAP XR Vector; ~5' adaptor sequence: 5' GAATTCGGACGAG 3' ~3' adaptor sequence: 5' CTCGAGTTTCTTTTCTTTT 3'"

ORIGIN

Query Match 4.3%; Score 38; DB 1; Length 361;
 Best Local Similarity 100.0%; Pred. No. 3.7e-08;
 Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 377 CCAGAGCCCCAGAAAACCCCTGGGCTCTGCTGAG 414
 DB 23 CCAGAGCCCCAGAAAACCCCTGGGCTCTGCTGAG 60

RESULT 8

AA791103 379 bp mRNA linear EST 06-FEB-1998
 LOCUS vW91a02.r1 Stratagene mouse skin (#937313) Mus musculus cDNA clone
 DEFINITION IMAGE:1229738 5', mRNA sequence.

ACCESSION AA791103
 VERSION AA791103.1 GI:2851223
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 379)
REFERENCE Mairre,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisler,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Stepcevic,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.
TITLE The WashU-HMI Mouse EST Project
JOURNAL Unpublished (1996)
COMMENT Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.edu
This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.lnl.gov) for further information.
MGI:555330
Seq primer: -28ml3 rev1 ET from Amersham
High quality sequence stop: 360.
Location/Qualifiers
1. .379
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:1229738"
/sex="females"
/tissue_type="whole skin"
/dev_stage="11 weeks old"
/lab_host="SOLR (kanamycin resistant)"
/clone_1b="Stratagene mouse skin (#937313)"
/note="Organ: skin; Vector: pluscript SK-; Site: 1; EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer: Oligo dT. Whole skin from 11 week old C57BL/6 female mice. Average insert size: 1.0 kb; Uni-ZAP XR Vector: -5' adaptor sequence: 5' GAAATCGGACGAG 3' -3' adaptor sequence: 5' CTCGAGTTTCTTTTCTTTT 3'."

ORIGIN
Query Match 4.3%; Score 38; DB 1; Length 379;
Best Local Similarity 100.0%; Pred. No. 3.7e-08;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 377 CCCAGCCCCGAGAAACCCCTGCGCTCTGCTGAG 414
Db 79 CCCAGCCCCGAGAAACCCCTGCGCTCTGCTGAG 116

RESULT 9
CG481452 416 bp DNA linear GSS 01-OCT-2003
LOCUS OST13885 Mus musculus 1295v/Ev Mus musculus genomic clone OST13885,
DEFINITION genomic survey sequence.
ACCESSION CG481452
VERSION CG481452.1 GI:37233834
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 416)
REFERENCE Zambrowicz,B.P., Abuin,A., Ramirez-Solis,R., Richter,L.J., Piggott,C.J., Beltrande,Rio,H., Buxton,E.C., Edwards,J., Finch,R.A., Fiddler,C.J., Gupta,A., Hansen,G., Hu,Y., Huang,W., Jang,C., Key,B.W., Jr., Klipp,P., Kohlhauf,B., Ma,Z.-Q., Markesich,D., Payne,R., Potter,D.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.-Z., Sparks,M.J., Van Sligtenhorst,I., Vogel,P., Walke,W., Xu,N., Zhu,Q., Person,C. and Sands,A.T.
TITLE Mki kinase deficiency lowers blood pressure in mice: a gene-trap

JOURNAL screen to identify potential targets for therapeutic intervention
Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
COMMENT Contact: Zambrowicz BP
OmniBank
Lexicon Genetics Incorporated
4000 Research Forest Drive, The Woodlands, TX 77381, USA
Email: materials@lexgen.com
Gene trap sequence tag generated by 3' RAGE from mouse ES cells as described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
Class: Gene trap.
Location/Qualifiers
1. .416
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="129Sv/Ev"
/db_xref="taxon:10090"
/clone="OST13885"
/cell_type="embryonic stem cell"
/clone_1b="Mus musculus 1295v/Ev"

ORIGIN
Query Match 4.3%; Score 38; DB 9; Length 416;
Best Local Similarity 100.0%; Pred. No. 3.7e-08;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 377 CCCAGCCCCGAGAAACCCCTGCGCTCTGCTGAG 414
Db 255 CCCAGCCCCGAGAAACCCCTGCGCTCTGCTGAG 292

RESULT 10
A1596929 422 bp mRNA linear EST 21-APR-1999
LOCUS VJ4611.y1 Stratagene mouse skin (#937313) Mus musculus cDNA clone
DEFINITION VJ4611.y1 Stratagene mouse skin (#937313) Mus musculus cDNA clone
ACCESSION A1596929
VERSION A1596929.1 GI:4605977
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 422)
REFERENCE Mairre,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Stepcevic,M., Theising,B., Allen,M., Bowles,M., Schurr,K., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Ralston,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Ralston,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
TITLE The WashU-NCI Mouse EST Project 1999
JOURNAL Unpublished (1999)
COMMENT Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.edu
This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.lnl.gov) for further information.
MGI:537028
This read is a RESSEQUENCE of a previously sequenced mouse clone
correct orientation)
Seq primer: -40RP from Gibco
High quality sequence stop: 396.
Location/Qualifiers
1. .422
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:932108"
/sex="females"
/tissue_type="whole skin"

Query Match
Best Local Similarity 100.0%; Score 38; DB 1; Length 422;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

377 CCCAGCCCCCAGAAAACCCCTGCTGCTGCTGCTGAG 414
|||||
282 CCCAGCCCCCAGAAAACCCCTGCTGCTGCTGCTGAG 319

dev_stage="11 weeks old"
/lab_host="SOLR (kanamycin resistant)"
/clone_1ib="Stratagene mouse skin (#937313)"
/note="Organ: skin; Vector: pBluescript SK-; Site 1:
ECORI; Site 2: XhoI; Cloned unidirectionally. Primer:
Oligo dt. Whole skin from 11 week old C57BL/6 female mice.
Average insert size: 1.0 kb; Uni-ZAP XR Vector; ~5'
adaptor sequence: 5' GAATTCGCGACGAG 3' ~3' adaptor
sequence: 5' CTCGAGTTTTTTTTTTTTTTTTTTT 3'"

ORIGIN

Query Match
Best Local Similarity 100.0%; Score 38; DB 1; Length 422;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

377 CCCAGCCCCCAGAAAACCCCTGCTGCTGCTGCTGAG 414
|||||
282 CCCAGCCCCCAGAAAACCCCTGCTGCTGCTGCTGAG 319

RESULT 11

CG487403 442 bp DNA linear GSS 01-OCT-2003
LOCUS OST22893 Mus musculus 129Sv/Ev Mus musculus genomic clone OST22893,
DEFINITION genomic survey sequence.
ACCESSION CG487403 GI:37246315
VERSION CG487403.1
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 442)
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Zambrowicz, B.P., Abuin, A., Ramirez-Solis, R., Richter, L.J.,
Fridolf, C.J., BeltrandelRio, H., Buxton, E.C., Edwards, J., Finch, R.A.,
Key, B.W., Jr., Kipp, P., Kohlhauff, B., Ma, Z.-Q., Markesich, D.,
Payne, R., Potter, D.G., Qian, N., Shaw, J., Schrick, J., Shi, Z.-Z.,
Sparks, M.U., Van Sligtenhorst, I., Vogel, P., Walke, W., Xu, N.,
Zhu, Q., Person, C. and Sands, A.T.
Mxl1 kinase deficiency lowers blood pressure in mice: a gene-trap
screen to identify potential targets for therapeutic intervention
Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)

AUTHORS

TITLE
JOURNAL
COMMENT
OmitBank
Lexicon Genetics Incorporated
4000 Research Forest Drive, The Woodlands, TX 77381, USA
Email: materials@lexgen.com
Gene trap sequence tag generated by 3' RAGE from mouse ES cells as
described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
Class: Gene Trap.

FEATURES

Location/Qualifiers
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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="129Sv/Ev"
/db_xref="taxon:10090"
/clone="OST22893"
/cell_type="embryonic stem cell"
/clone_1ib="Mus musculus 129Sv/Ev"

ORIGIN

Query Match
Best Local Similarity 100.0%; Score 38; DB 9; Length 442;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 377 CCCAGCCCCCAGAAAACCCCTGCTGCTGCTGCTGAG 414
|||||
Db 239 CCCAGCCCCCAGAAAACCCCTGCTGCTGCTGCTGAG 276

RESULT 12

AA798896

LOCUS AA798896 451 bp mRNA linear EST 10-FEB-1998
DEFINITION v94e08.t1 Stratagene mouse skin (#937313) Mus musculus cDNA clone
IMAGE:1230086 5', mRNA sequence.
AA798896
ACCESSION AA798896.1 GI:2861851
VERSION
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE

1 (bases 1 to 451)
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Treisinger, R., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
Waterston, R.
The WashU-HMNI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HMNI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.edu
This clone is available royalty-free through LBNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:655678

JOURNAL

Putative full length read
vector to vector length is 671
Seq primer: -28ml3 rev1 ET from Amersham
High quality sequence stop: 431.
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1..451
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/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:1230086"
/sex="females"
/issue_type="whole skin"
/dev_stage="11 weeks old"
/lab_host="SOLR (kanamycin resistant)"
/clone_1ib="Stratagene mouse skin (#937313)"
/note="Organ: skin; Vector: pBluescript SK-; Site 1:
ECORI; Site 2: XhoI; Cloned unidirectionally. Primer:
Oligo dt. Whole skin from 11 week old C57BL/6 female mice.
Average insert size: 1.0 kb; Uni-ZAP XR Vector; ~5'
adaptor sequence: 5' GAATTCGCGACGAG 3' ~3' adaptor
sequence: 5' CTCGAGTTTTTTTTTTTTTTTTTTT 3'"

FEATURES

Location/Qualifiers
1..451
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:1230086"
/sex="females"
/issue_type="whole skin"
/dev_stage="11 weeks old"
/lab_host="SOLR (kanamycin resistant)"
/clone_1ib="Stratagene mouse skin (#937313)"
/note="Organ: skin; Vector: pBluescript SK-; Site 1:
ECORI; Site 2: XhoI; Cloned unidirectionally. Primer:
Oligo dt. Whole skin from 11 week old C57BL/6 female mice.
Average insert size: 1.0 kb; Uni-ZAP XR Vector; ~5'
adaptor sequence: 5' GAATTCGCGACGAG 3' ~3' adaptor
sequence: 5' CTCGAGTTTTTTTTTTTTTTTTTTT 3'"

ORIGIN

Query Match
Best Local Similarity 100.0%; Score 38; DB 1; Length 451;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 377 CCCAGCCCCCAGAAAACCCCTGCTGCTGCTGCTGAG 414
|||||
Db 177 CCCAGCCCCCAGAAAACCCCTGCTGCTGCTGCTGAG 214

RESULT 13

CG484009 451 bp DNA linear GSS 01-OCT-2003
LOCUS OST17807 Mus musculus 129Sv/Ev Mus musculus genomic clone OST17807,
DEFINITION genomic survey sequence.
ACCESSION CG484009 GI:37239343
VERSION CG484009.1
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 451)
 AUTHORS Zambrowicz,B.P., Abuin,A., Ramirez-Solis,R., Richter,L.J.,
 Pigott,J., Beltrande,Rio,H., Buxton,E.C., Edwards,J., Finch,R.A.,
 Fiddle,C.J., Gupta,A., Hansen,G., Hu,Y., Huang,W., Jiang,C.,
 Kay,B.W., Jr., Kipp,P., Konhauft,B., Ma,Z.-Q., Markesich,D.,
 Payne,R., Potter,D.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.-Z.,
 Sparks,M.J., Van Sligtenhorst,I., Vogel,P., Walke,W., Xu,N.,
 Zhu,Q., Person,C. and Sands,A.T.
 Mki kinase deficiency lowers blood pressure in mice: a gene-trap
 screen to identify potential targets for therapeutic intervention
 Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
 COMMENT Contact: Zambrowicz BP
 OmniBank
 Lexicon Genetics Incorporated
 4000 Research Forest Drive, The Woodlands, TX 77381, USA
 Email: materials@lexgen.com
 Gene trap sequence tag generated by 3' RAGE from mouse ES cells as
 described in Zambrowicz et al (Nature, 1998 Apr 9;392(6676):608-11)
 Class: Gene Trap.
 Location/Qualifiers
 1..451
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="129Sv/Ev"
 /db_xref="taxon:10090"
 /clone="OST17807"
 /cell_type="embryonic stem cell"
 /clone_id="Mus musculus 129Sv/Ev"

ORIGIN
 Query Match 4.3%; Score 38; DB 9; Length 451;
 Best Local Similarity 100.0%; Pred. No. 3.7e-08;
 Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 377 CCAGCCCCCAGAAACCCTGCGCTCTCTGCTGAG 414
 256 CCAGCCCCCAGAAACCCTGCGCTCTCTGCTGAG 293

Db
 RESULT 14 489 bp DNA linear GSS 19-JUL-2001
 LOCUS BH098389/c
 DEFINITION RPCI-24-372N23_TV RPCI-24 Mus musculus genomic clone
 RPCI-24-372N23, genomic survey sequence.
 ACCESSION BH098389
 VERSION BH098389.1 GI:14920132
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 489)
 Zhao,S., Nierman,W., Malek,J., Shateman,S., Akinret,B., Levins,M.,
 Tsegaye,G., Geer,K., Krol,M., Shvartsbeyn,A., Gebregeorgis,B.,
 Russell,D., de Jong,P. and Fraser,C.M.
 Mouse BAC End Sequences from Library RPCI-24
 Unpublished (1999)
 TITLE Contact: Shaying Zhao
 JOURNAL Department of Eukaryotic Genomics
 COMMENT The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: szhao@tigr.org
 Clones are derived from the mouse BAC library RPCI-24. For BAC
 library availability, please contact Pieter de Jong
 (pdejong@mail.cho.org). Clones may be purchased from BACPAC
 Resources (http://www.choi.org/bacpac/orderingframe.htm). BAC end
 page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
 Plate: 372 row: N column: 23
 Seq primer: T7
 Class: BAC ends.
 Location/Qualifiers

source 1..489
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 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="RPCI-24-372N23"
 /sex="Male"
 /cell_type="Spleen/Brain"
 /clone_id="RPCI-24"
 /note="Vector: pTARBAC1; Site 1: BamHI; Site 2: BamHI;
 RPCI-24 Mouse BAC library produced by Pieter de Jong. The
 library was cloned in the pTARBAC1 cloning vector at the
 BamHI sites using MboI partially digested male C57BL/6J
 DNA."

ORIGIN
 Query Match 4.3%; Score 38; DB 8; Length 489;
 Best Local Similarity 100.0%; Pred. No. 3.7e-08;
 Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 377 CCAGCCCCCAGAAACCCTGCGCTCTCTGCTGAG 414
 Db 447 CCAGCCCCCAGAAACCCTGCGCTCTCTGCTGAG 410

RESULT 15 562 bp mRNA linear EST 22-JUL-1997
 LOCUS AA530301
 DEFINITION VJ46el1.r1 Stragene mouse skin (#937313) Mus musculus cDNA clone
 VJ46el1:932108 5', mRNA sequence.
 ACCESSION AA530301
 VERSION AA530301.1 GI:2273007
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 562)
 Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
 Geisel,S., Kucada,T., Lacy,M., Le,M., Martin,J., Morris,M.,
 Scheinberg,K., Stepcoe,M., Tan,F., Underwood,K., Moore,B.,
 Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
 Waterston,R.
 The WashU-HMI Mouse EST Project
 Unpublished (1996)
 TITLE Contact: Marra M/Mouse EST Project
 JOURNAL WashU-HMI Mouse EST Project
 COMMENT Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@watson.wustl.edu
 This clone is available royalty-free through LNL; contact the
 IMAGS Consortium (info@image.lnl.gov) for further information.
 MGI:537028
 Seq primer: -28m13 rev1 ET from Amersham
 High quality sequence stop: 221.
 Location/Qualifiers
 1..562
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6"
 /db_xref="taxon:10090"
 /clone="IMAGE:932108"
 /sex="females"
 /tissue_type="whole skin"
 /dev_stage="11 weeks old"
 /lab_host="SOLR (kanamycin resistant)"
 /clone_id="Stragene mouse skin (#937313)"
 /note="Organ: skin; Vector: pBluescript SK-; Site 1:
 EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer:
 Oligo dt. Whole skin from 11 week old C57BL/6 female mice.
 Average insert size: 1.0 kb; Uni-ZAP XR Vector; ~5'

adaptor sequence: 5' GAATCGGACGAG 3' ~3' adaptor
 sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3' "

Query Match 4.3%; Score 38; DB 1; Length 562;
 Best local Similarity 100.0%; Pred. No. 3.7e-08;
 Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 377 CCCAGCCCCCAGAAAAACCCCTGCGCCCTCCTGCGCCCTGAG 414
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 Db 281 CCCAGCCCCCAGAAAAACCCCTGCGCCCTCCTGCGCCCTGAG 318

Search completed: January 11, 2005, 11:38:28
 Job time : 3420 secs


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Db      124  GACGACCTTGCGCGGAGAGACCCCGAGCCCGCCAGAAACCCCTGSCCT 65
Qy      117  GluValAspAaAaArgProGIuGIuProAaPleuAaPProAaArgIuIyYArg 136
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RESULT 2
US-09-103-840A-2/c
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2
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GenCore version 5.1.6
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OM protein - nucleic search, using frame_p2n model

Run on: January 11, 2005, 11:50:49 : Search time 489.056 Seconds
(without alignments)
1595.608 Million cell updates/sec

Title: US-09-994-365-2

Perfect score: 808

Sequence: 1 MLNWLKILVLCIHTRGI.....EVDNRQBPBDDLPREXER 136

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4293498 segs, 2868903791 residues

Total number of hits satisfying chosen parameters: 8586996

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-Q=cgnt2_1/USPTO.spool.h/US0994365/runat_10012005.172233.6861/app.query.fasta_1.590
-DB=Published.Applications.NA -QFMT=fastap -SUFFIX=p2n.rmpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bases -START=1 -END=1 -MARRIX-blobsum62
-TRANS-human40.csl -LIST=45 -DOCCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=local -OUTFMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US0994365 @CGN_1_1_582 @runat_10012005.172233.6861
-NCPU=6 -ICPU=3 -NO MMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
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Database :

Published Applications_NA:*

- 1: /cgnt2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /cgnt2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgnt2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 4: /cgnt2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
- 5: /cgnt2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
- 6: /cgnt2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
- 7: /cgnt2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 8: /cgnt2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 9: /cgnt2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
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- 11: /cgnt2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgnt2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
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- 18: /cgnt2_6/ptodata/2/pubpna/US10F_NEW_PUB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

*

Result No.	Score	Query Match	Length	DB ID	Description
1	808	100.0	891	9 US-09-994-365-1	Sequence 1, Appl
2	712	88.1	2997	9 US-09-994-365-10	Sequence 10, Appl
3	712	88.1	3001	9 US-09-994-365-4	Sequence 4, Appl
4	712	88.1	25235	15 US-10-164-230-2	Sequence 2, Appl
5	712	88.1	55050	17 US-10-467-752-4	Sequence 4, Appl
6	486	60.1	565	15 US-10-029-386-5700	Sequence 5700, Ap
7	449	55.6	367378	15 US-10-312-861-1	Sequence 1
8	314	38.9	157	15 US-10-029-386-19510	Sequence 19510, A
9	199	24.6	711	16 US-10-282-122A-31860	Sequence 31860, A
10	198.5	24.6	2772	16 US-10-282-122A-28290	Sequence 28290, A
11	197	24.4	573	17 US-10-767-701-4301	Sequence 4301, Ap
12	196	24.3	766	18 US-10-425-115-82176	Sequence 82176, A
13	195.5	24.2	446	9 US-09-864-761-20659	Sequence 20659, A
14	195	24.1	12733	14 US-10-032-393-47	Sequence 47, Appl
15	195	24.1	12739	14 US-10-032-393-8	Sequence 8, Appl
16	191	23.9	985	18 US-10-425-115-91623	Sequence 91623, A
17	191	23.6	426	17 US-10-021-323-5998	Sequence 5998, Ap
18	190	23.5	916	18 US-10-425-115-47293	Sequence 47293, A
19	189.5	23.5	815	16 US-10-424-599-20495	Sequence 20495, A
20	189	23.4	925	17 US-10-437-963-44536	Sequence 44536, A
21	188.5	23.3	600	18 US-10-363-345A-39087	Sequence 39087, A
22	188.5	23.3	600	18 US-10-363-345A-39088	Sequence 39088, A
23	188	23.3	545	17 US-10-437-963-56258	Sequence 56258, A
24	188	23.3	1493	15 US-10-029-386-25133	Sequence 25133, A
25	187.5	23.2	1327	16 US-10-398-221-1265	Sequence 1265, Ap
26	186.5	23.1	629	17 US-10-021-323-9375	Sequence 9375, Ap
27	186.5	23.1	821	18 US-10-425-115-131043	Sequence 131043, A
28	186	23.0	700	18 US-10-425-115-14077	Sequence 14077, A
29	186	23.0	1455	16 US-10-282-122A-28683	Sequence 28683, A
30	185.5	23.0	588	17 US-10-021-323-9377	Sequence 9377, Ap
31	185.5	23.0	1245	17 US-10-437-963-94850	Sequence 94850, A
32	185.5	23.0	1744	17 US-10-437-963-19774	Sequence 19774, A
33	184.5	22.8	485	16 US-10-424-599-65670	Sequence 65670, A
34	184	22.8	882	17 US-10-437-963-28390	Sequence 28390, A
35	183.5	22.7	3163	15 US-10-017-161-1857	Sequence 1857, Ap
36	183.5	22.7	3163	15 US-10-292-798-1513	Sequence 1513, Ap
37	183	22.6	590	18 US-10-425-115-133228	Sequence 133228, A
38	182.5	22.6	415	17 US-10-021-323-12908	Sequence 12908, A
39	182.5	22.6	659	17 US-10-767-701-4135	Sequence 4135, Ap
40	182.5	22.6	823	18 US-10-425-115-53676	Sequence 53676, A
41	182.5	22.6	965	15 US-10-029-386-22737	Sequence 22737, A
42	182.5	22.6	1083	15 US-10-029-386-20723	Sequence 20723, A
43	182.5	22.6	2862	9 US-09-888-615-7	Sequence 7, Appl
44	182.5	22.6	3067	16 US-10-311-035-42	Sequence 42, Appl
45	182	22.5	457	16 US-10-424-599-133788	Sequence 133788, A

ALIGNMENTS

RESULT 1
US-09-994-365-1
Sequence 1, Application US/0994365
Patent No. US20020115148A1
GENERAL INFORMATION:
APPLICANT: Charmley, Patrick
APPLICANT: Moss, Patrick
APPLICANT: McBluen, Mark
TITLE OF INVENTION: Compositions and Methods for Diagnosing or Treating Prioriasis
FILE REFERENCE: CECH118109
CURRENT APPLICATION NUMBER: US/09/994,365
CURRENT FILING DATE: 2001-11-26
PRIOR APPLICATION NUMBER: US 60/253,592
PRIOR FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: US 60/256,839
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1
LENGTH: 891
TYPE: DNA

ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (64) .. (471)
US-09-994-365-1

Alignment Scores:
Pred. No.: 6,33e-61 Length: 891
Score: 808.00 Matches: 136
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-994-365-2 (1-136) x US-09-994-365-1 (1-891)

QY 1 MetIleuAenTPrLyLeuG[Y]LeuValIeuYsLeuH1gThrArG[Y]Ile 20
DB 64 ATGATCTCTCAAGAGCTCTGAGATCTGATCTGCTTGTCTGCAACCAAGAGGATC 123
QY 21 SerGlySerGluGlyH1sProSerH1sProAlaGluAspArgGluGluAlaGlySer 40
DB 124 TCAAGCAGCGAGGCGCAACCCCTTCAACCCAGACGAGACGAGAGGCGAGGCTCC 183
QY 41 ProThiLeuProGluGlyProProValProGlyAspProTTPProGlyAlaProLeu 60
DB 184 CCAACATGCTCTCAGGGGCCCCCAGTCCCGGTGACCTTGCGCAGGGGCAACCCCTCTC 243
QY 61 PheGluAspProProProThiArgProSerArgProTTPArgAspLeuProGluThrGly 80
DB 244 TTGAAATCTCTCGGCTTACCGGCCAGATGTCCTCGAGAGACCTGCTGAAACTGGA 303
QY 81 ValTTPProProGluProProArgThiAspProProGluProProArgProAspAspPro 100
DB 304 GTCTGGCCCCCTGAACCGCTAGAACGATCTCTCACTCCCGGCTGAGACCT 363
QY 101 TrpProAlaGlyProGluProProGluAspProTTPProProAlaProGluAlaAspAsn 120
DB 364 TGGCGGCGAGAGCCCGCCAGAACCCCTGAGGCTCTGAGGTGAGCAAC 423
QY 121 ArgProGluGluGluProAspLeuAspProProArgGluGluTyrArg 136
DB 424 CGAACCTAGAGAGAGCCAGACTTGAACCCCGGAGAAAGTACAGA 471

RESULT 2
US-09-994-365-10
Sequence 10, Application US/09994365
Patent No. US20020115148A1
GENERAL INFORMATION:
APPLICANT: Charmley, Patrick
APPLICANT: Moss, Patrick
APPLICANT: McEuen, Mark
TITLE OF INVENTION: Compositions and Methods for Diagnosing or Treating Psoriasis
FILE REFERENCE: CECH18109
CURRENT APPLICATION NUMBER: US/09/994,365
CURRENT FILING DATE: 2001-11-26
PRIOR APPLICATION NUMBER: US 60/253,592
PRIOR FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: US 60/256,839
PRIOR FILING DATE: 2000-12-15
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn version 3.0
SEQ ID NO 10
LENGTH: 2997
TYPE: DNA
ORGANISM: Homo sapiens
US-09-994-365-10

Alignment Scores:
Pred. No.: 3.15e-52 Length: 2997
Score: 712.00 Matches: 118
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Mismatch: 0

Query Match: 88.12% Indels: 0
DB: 9 Gaps: 0

US-09-994-365-2 (1-136) x US-09-994-365-10 (1-2997)

QY 19 GlyTLeSerGlySerGluGlyH1sProSerH1sProAlaGluAspArgGluGluAla 38
DB 2201 GGCACTTCAGAGCAGGAGGCGCAACCCCTTCAACCCAGACCGAGAGCGAGAGGCA 2260
QY 39 GlySerProThiLeuProGluGlyProProValProGlyAspProTTPProGlyAlaPro 58
DB 2261 GGCTCCCAACATGCTCTCAGGGGCCCCCAGTCCCGGTGACCTTGGCCAGGGGCAACC 2320
QY 59 ProLeuPheGluAspProProProThiArgProSerArgProTTPArgAspLeuProGlu 78
DB 2321 CTTCTTGAATCTCTCGGCTTACCGGCCAGATGTCCTCGAGAGACCTGCTGAA 2380
QY 79 ThrGlyValTTPProProGluProProArgThiAspProProGluProProArgProAsp 98
DB 2381 ACTGAGTCTGGCCCCCTGAACCGCTAGAACGATCTCTCACTCCCGGCTGAC 2440
QY 99 AspProTTPProAlaGlyProGluProProGluAspProTTPProProAlaProGluAla 118
DB 2441 GACCTTGGCGGCGAGAGCCCGCCAGAACCCCTGAGCTCTGCTGCTGAGGTG 2500
QY 119 AspAsnArgProGluGluGluProAspLeuAspProProArgGluGluTyrArg 136
DB 2501 GACAACTGACCTCAGAGAGAGCCAGACTTGAACCCCGGAGAAAGTACAGA 2554

RESULT 3
US-09-994-365-4
Sequence 4, Application US/09994365
Patent No. US20020115148A1
GENERAL INFORMATION:
APPLICANT: Charmley, Patrick
APPLICANT: Moss, Patrick
APPLICANT: McEuen, Mark
TITLE OF INVENTION: Compositions and Methods for Diagnosing or Treating Psoriasis
FILE REFERENCE: CECH18109
CURRENT APPLICATION NUMBER: US/09/994,365
CURRENT FILING DATE: 2001-11-26
PRIOR APPLICATION NUMBER: US 60/253,592
PRIOR FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: US 60/256,839
PRIOR FILING DATE: 2000-12-15
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn version 3.0
SEQ ID NO 4
LENGTH: 3001
TYPE: DNA
ORGANISM: Homo sapiens
US-09-994-365-4

Alignment Scores:
Pred. No.: 3.16e-52 Length: 3001
Score: 712.00 Matches: 118
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 88.12% Indels: 0
DB: 9 Gaps: 0

US-09-994-365-2 (1-136) x US-09-994-365-4 (1-3001)

QY 19 GlyTLeSerGlySerGluGlyH1sProSerH1sProAlaGluAspArgGluGluAla 38
DB 2205 GGCACTTCAGAGCAGGAGGCGCAACCCCTTCAACCCAGACCGAGAGCGAGAGGCA 2264
QY 39 GlySerProThiLeuProGluGlyProProValProGlyAspProTTPProGlyAlaPro 58
DB 2265 GGCTCCCAACATGCTCTCAGGGGCCCCCAGTCCCGGTGACCTTGGCCAGGGGCAACC 2324
QY 59 ProLeuPheGluAspProProProThiArgProSerArgProTTPArgAspLeuProGlu 78

Db 2325 CCTCTTTGAAAGATCTCCGCTACCCGCCAGTCGTCCCTGAGAGACTTGCCTGAA 2384
Qy 79 ThrglyValTrpProGluProProArgThrAspProGlnProProArgProAsp 98
Db 2385 ACTGGAGTCTGGCCCCCTGAAACCGCTTAGAACGATCTCTCAACTCCCCGGCCTGAC 2444
Qy 99 AspProTrpProAlaGlyProGlnProProGluAsnProTrpProProAlaProGluVal 118
Db 2445 GACCCCTGGCCGGCAGAGACCCCGACAAAACCCCTGCTCTGCTGCTGAGGTG 2504
Qy 119 AspAsnArgProGlnGluGluProAspLeuAspProProAlaGlyGluTrpArg 136
Db 2505 GACAACCGACTCGAGAGACCGACTAGACCACCCCGGAAGATCAGA 2558

RESULT 4
US-10-164-230-2
; Sequence 2, Application US/10164230
; Publication No. US20030170652A1
; GENERAL INFORMATION:
; APPLICANT: Inoko, Hidetoshi
; APPLICANT: Tamiva, Gen
; TITLE OF INVENTION: METHOD OF TESTING FOR PSORIASIS VULGARIS
; FILE REFERENCE: 06501-112US1
; CURRENT APPLICATION NUMBER: US/10/164,230
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: PCT/JP00/08624
; PRIOR FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: JP 11/346867
; PRIOR FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 25235
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: exon
; LOCATION: (1) ... (420)
; FEATURE:
; NAME/KEY: exon
; LOCATION: (1282) ... (1405)
; FEATURE:
; NAME/KEY: exon
; LOCATION: (1602) ... (1702)
; FEATURE:
; NAME/KEY: exon
; LOCATION: (1602) ... (1631)
; FEATURE:
; NAME/KEY: exon
; LOCATION: (2352) ... (2364)
; FEATURE:
; NAME/KEY: exon
; LOCATION: (6287) ... (6509)
; FEATURE:
; NAME/KEY: exon
; LOCATION: (10417) ... (10493)
; FEATURE:
; NAME/KEY: exon
; LOCATION: (14244) ... (14407)
; FEATURE:
; NAME/KEY: exon
; LOCATION: (14244) ... (14344)
; FEATURE:
; NAME/KEY: exon
; LOCATION: (25190) ... (25235)
; US-10-164-230-2

Alignment Scores:
Pred. No.: 1,85e-51 Length: 25235
Score: 712.00 Matches: 118
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 88.12% Indels: 0

DB: 15 Gaps: 0
US-09-994-365-2 (1-136) x US-10-164-230-2 (1-25235)
Qy 19 GlyIleSerGlySerGluGlyHisProSerHisProProAlaGluAspArgGluVal 38
Db 1754 GGCATCTCAGACGACGAGGCGCACCCCTCTCACACCCGACGAGACCGAGAGAGCA 1813
Qy 39 GlySerProThrLeuProGlnGlyProProValProGlyAspProTrpProGlyValPro 58
Db 1814 GGCCTCCCAACATTGCTCTAGGGCCCCCAGTCCCCCGATACCTTGCCAGGGGCAACC 1873
Qy 59 ProLeuHegLubAspProProProThrArgProSerArgProTrpArgAspLeuProGlu 78
Db 1874 CCTCTTTGAAAGATCTCCGCTACCCGCCCGCAGTGTCTCTGAGAGACTTGCCTGAA 1933
Qy 79 ThrglyValTrpProGluProProArgThrAspProGlnProProAlaProGluVal 118
Db 1934 ACTGGAGTCTGGCCCCCTGAAACCGCTTAGAACGATCTCTCAACTCCCCGGCCTGAC 1993
Qy 99 AspProTrpProAlaGlyProGlnProProGluAsnProTrpProProAlaProGluVal 118
Db 1994 GACCCCTGGCCGGCAGAGACCCCGACCCCGAAGAACCCCTGCTCTGCTGAGGTG 2053
Qy 119 AspAsnArgProGlnGluGluProAspLeuAspProProAlaGlyGluTrpArg 136
Db 2054 GACAACCGACTCGAGAGACCGACTAGACCACCCCGGAAGATCAGA 2107

RESULT 5
US-10-467-752-4
; Sequence 4, Application US/10467752
; Publication No. US20040161759A1
; GENERAL INFORMATION:
; APPLICANT: Lench, et al.
; TITLE OF INVENTION: Test and Model for Inflammatory disease
; FILE REFERENCE: 2003882-0009
; CURRENT APPLICATION NUMBER: US/10/467,752
; CURRENT FILING DATE: 2003-08-13
; PRIOR APPLICATION NUMBER: PCT/GB02/00653
; PRIOR FILING DATE: 2002-02-13
; PRIOR APPLICATION NUMBER: GB0103514.6
; PRIOR FILING DATE: 2001-02-13
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 55050
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (13351) ... (13351)
; OTHER INFORMATION: n i s a o r t o r g o r c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (13401) ... (13401)
; OTHER INFORMATION: n i s a o r t o r g o r c
; US-10-467-752-4

Alignment Scores:
Pred. No.: 3.54e-51 Length: 55050
Score: 712.00 Matches: 118
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 88.12% Indels: 0
DB: 17 Gaps: 0

US-09-994-365-2 (1-136) x US-10-467-752-4 (1-55050)
Qy 19 GlyIleSerGlySerGluGlyHisProSerHisProProAlaGluAspArgGluVal 38
Db 2709 GGCATCTCAGACGACGAGGCGCACCCCTCTCACACCCGACGAGACCGAGAGAGCA 27158
Qy 39 GlySerProThrLeuProGlnGlyProProValProGlyAspProTrpProGlyValPro 58

Db 27159 GGCCTCCCAACATGCTCCAGGGGCCCCAGTCCCGGTGACCTTGAGCCAGGGGACACC 27218
Qy 59 ProleuphegluaspProProProThArPProSerArpProTPARgAspleuProglu 78
Db 27219 CTTCTCTTTGAAGATCTCTCGGCTTACCGGCCGATGTCCTGGAAGAGACTGCTGAA 27278
Qy 79 ThrGlyValTrpProProgluProProArGThrAspProProgluProProArGProasp 98
Db 27279 ACTGAGTCTGCGCCCTGAAACCGCTAGAACGGATCTCTCAACTCCCGGCTGAC 27338
Qy 99 AspProTrpProAlaGlyProProgluProProgluAsnProTrpProAlaProgluVal 118
Db 27339 GACCCCTTGCGCGGAGAGACCCGACCCCAAAAACCCCTGCTCTGCGCCCTGAGGTG 27398
Qy 119 AspAsnArpProgluIngluProAspleuAspProProArGluInuTrArg 136
Db 27399 GACACCGACCTCAGAGAGAGACCACTAGACCCACCCGAGAGAGTACAGA 27452

RESULT 6
US-10-029-386-5700
; Sequence 5700, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:

; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
; TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
; FILE REFERENCE: AEWICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 5700
; LENGTH: 565
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AB023060.1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.82
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.82
; OTHER INFORMATION: SWISSPROT HIT: Q99715, EVALUE 6.20e-01
; OTHER INFORMATION: EST HUMAN HIT: BF513178.1, EVALUE 0.00e+00
; OTHER INFORMATION: NT HIT: g115304354, EVALUE 0.00e+00
US-10-029-386-5700

Alignment Scores:

Pred. No.:	2.2e-33	Length:	565
Score:	486.00	Matches:	79
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	60.15%	Indels:	0
DB:	15	Gaps:	0

US-09-994-365-2 (1-136) x US-10-029-386-5700 (1-565)

Qy 58 ProProleuphegluaspProProProThArPProSerArpProTPARgAspleuPro 77
Db 1 CCCCCTCTCTTTGAAGATCTCTCGGCTTACCGGCCGATGTCCTGGAAGAGACTGCT 60
Qy 78 GluThrGlyValTrpProProgluProProArGThrAspProProgluProProArGPro 97
Db 61 GAAACTGAGTCTGCGCCCTGAAACCGCTAGAACGGATCTCTCAACTCCCGGCT 120
Qy 98 AspAspProTrpProAlaGlyProProgluProProgluAsnProTrpProAlaProglu 117
Db 121 GAGGACCTTTGGCCGAGAGACCCGACCCCAAAAACCCCTGCGCTCTGCTGAG 180
Qy 118 ValAspAsnArpProgluIngluProAspleuAspProProArGluInuTrArg 136
Db 181 GTGGACACCGACCTCAGAGAGAGACCACTAGACCCACCCGAGAGAGTACAGA 237

RESULT 7

US-10-312-841-1/c
; Sequence 1, Application US/10312841
; Publication No. US20030186277A1
; GENERAL INFORMATION:
; APPLICANT: Epigenomics AG
; TITLE OF INVENTION: Diagnose von bedeutenden genetischen Parametern innerhalb des HNC
; FILE REFERENCE: E01/1208/MO
; CURRENT APPLICATION NUMBER: US/10/312,841
; CURRENT FILING DATE: 2002-12-30
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 1
; LENGTH: 3673778
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; NAME/KEY: unsure
; LOCATION: (3294164)
US-10-312-841-1

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus.p2n model

Run on: January 11, 2005, 09:34:16 ; Search time 362.064 Seconds
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Title: US-09-994-365-3

Perfect score: 692

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Fgapop 6.0 , Fgapext 7.0	
Delpop 6.0 , Delpext 7.0	

Searched: 413486 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELDP=6 -DELEXT=7

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11: geneseqn2003ds.*
12: geneseqn2004s.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	692	100.0	891	6	ABK86962 Human can
2	692	100.0	1473	6	ABN60006 Novel hum
3	692	100.0	2997	6	ABK86967 Human CAN
4	692	100.0	3001	6	ABK86963 Human CAN
5	692	100.0	25235	4	AAH45310 Human SEE
6	692	100.0	55050	6	ABQ75680 Human SEE

7	486	70.2	565	12	ACH72505	Ach72505 Human gen
8	314	45.4	157	12	ACH86315	Ach86315 Human gen
9	199	28.8	711	8	ACA43990	ACA43990 Prokaryot
10	198.5	28.7	2772	8	ACA04020	ACA04020 Prokaryot
11	198.5	28.7	110000	4	AAI99682_10	Continuation (11 o
12	198.5	28.7	110000	4	AAI99682_10	Continuation (11 o
13	190.5	27.5	446	4	AAI23276	AAI23276 Probe #13
14	190.5	27.5	446	4	ABA68382	ABA68382 Human foe
15	190.5	27.5	446	4	AAI48596	AAI48596 Probe #17
16	190.5	27.5	446	4	ABA50433	ABA50433 Human bre
17	190.5	27.5	446	4	ABA35379	ABA35379 Probe #13
18	190.5	27.5	446	4	AAK42529	AAK42529 Human bon
19	190.5	27.5	446	4	AAK16757	AAK16757 Human bra
20	190.5	27.5	446	4	ABSA2140	ABSA2140 Human liv
21	190.5	27.5	446	5	AAI08921	AAI08921 Probe #89
22	190.5	27.5	446	6	ABS16574	ABS16574 Human gen
23	188.5	27.2	600	6	ABQ52497	ABQ52497 Oligonuc1
24	188.5	27.2	110000	4	AAI99682_09	Continuation (10 o
25	188.5	27.2	110000	4	AAI99682_27	Continuation (28 o
26	188.5	27.2	110000	4	AAI99682_28	Continuation (29 o
27	188.5	27.2	110000	4	AAI99682_28	Continuation (29 o
28	188.5	27.2	110000	4	AAI99682_09	Continuation (28 o
29	188.5	27.2	110000	4	AAI99682_27	Continuation (28 o
30	188	27.2	1493	12	ACH91938	Ach91938 Human gen
31	187.5	27.1	1327	6	ABQ68452	ABQ68452 Listeria
32	187.5	27.1	3946	8	AAT93610	AAT93610 Mycobacte
33	186	26.9	1452	8	ACR93617	ACR93617 Mycobacte
34	186	26.9	1455	8	ACA00813	ACA00813 Prokaryot
35	186	26.9	12733	6	ABK98631	ABK98631 Vector pb
36	186	26.9	12733	6	ACD13882	ACD13882 L. lactis
37	186	26.9	12739	6	ABK98592	ABK98592 Vector pb
38	186	26.9	12739	6	ACD13843	ACD13843 Plasmid p
39	186	26.9	110000	4	AAI99682_37	Continuation (38 o
40	186	26.9	110000	4	AAI99682_37	Continuation (38 o
41	184	26.6	7720	3	AAAS5800	Aaas5800 Genomic D
42	184	26.6	110000	4	AAI99682_11	Continuation (12 o
43	183.5	26.5	3163	10	ADCB7060	Adcb7060 Human GPC
44	183	26.4	1833	4	ABL22159	ABL22159 Drosophila
45	183	26.4	110000	4	AAI99682_39	Continuation (40 o

ALIGNMENTS

RESULT 1	
ABK86962	ABK86962 standard; cDNA; 891 BP.
ID	ABK86962;
AC	ABK86962;
XX	
DT	24-SEP-2002 (first entry)
XX	
DE	Human candidate coding sequence-1 (CAN-1) cDNA.
XX	
KW	Human; antiposoriatic; chromosome 6; candidate coding sequence-1; CAN-1;
KW	SEER-1; STG; human leukocyte antigen C; HLA C; HLA Cw6; psoriasis; skin;
KW	keratinocyte; chronic inflammatory dermatosis; erythroderma; seborrheic;
KW	gutrate; pustular variant; Reiter's disease; hyperproliferation;
KW	epidermis; differentiation; diagnosis; gene therapy; gene; ss; SNP;
XX	single nucleotide polymorphism.
OS	Homo sapiens.
XX	
Key	Location/Qualifiers
FT	64..474
FT	/*tag= a
FT	/product= "CAN-1"
FT	64..129
FT	sig_peptide
FT	/*tag= b
FT	130..471
FT	/*tag= c
FT	/note= "Mature CAN-1"
FT	replace(311,C)
FT	variation
FT	/*tag= d

XX	FT	standard_name= "single nucleotide polymorphism"
XX	PN	
XX	XX	WO20024375-A2.
XX	XX	
XX	PD	06-JUN-2002.
XX	XX	
XX	PF	27-NOV-2001; 2001WO-US044506.
XX	XX	
XX	PR	28-NOV-2000; 2000US-0253592P.
XX	PR	15-DEC-2000; 2000US-0256639P.
XX	XX	
XX	PA	(CELL-) CELLTECH R & D INC.
XX	XX	
XX	PI	Charmley P, Moss P, Mceuen M;
XX	XX	
XX	DR	WPI; 2002-508513/54.
XX	DR	P-PSDB; AAU79579.
XX	XX	
XX	PT	Novel isolated CAN-1 polypeptide involved in keratinocyte proliferation
XX	PT	and differentiation, and polynucleotides encoding the polypeptide, useful
XX	PT	for diagnosing or predicting susceptibility to psoriasis in individual.
XX	XX	
XX	XX	Claim 8; Page 80-81; 95pp; English.
XX	XX	

CC The invention discloses isolated candidate coding sequence-1 (CAN-1),
CC SEEK-1 (not defined) and STG (not defined) polypeptides, and the
CC polynucleotides encoding them. All three genes were identified due to
CC their proximity to the human leukocyte antigen C (HLA C) locus on
CC chromosome 6. The HLA Cw6 allele is associated with psoriasis and as the
CC three genes are expressed in normal skin and/or keratinocyte tissue, they
CC may also have a role in psoriasis. Psoriasis is a chronic inflammatory
CC dermatosis that is characterized by hyperproliferation of epidermal
CC cells. Possible treatments against psoriasis involve the inhibition of
CC movement of cells into the epidermis, or the inhibition of
CC hyperproliferation or abnormal differentiation of keratinocytes, by the
CC inhibition of the CAN-1, STG or SEEK-1 polypeptides binding to their
CC binding partners. The polypeptides are useful for diagnosing or
CC predicting the susceptibility to psoriasis in an individual, for
CC ameliorating the symptoms and/or progression of psoriasis and for
CC identifying agents useful for treating psoriasis or modulating the
CC activity of the polypeptide. The polypeptides are also useful for
CC enhancing the level of CAN-1, STG or SEEK-1 biological activity in a cell
CC or tissue. The nucleic acid molecules are useful as hybridisation probes
CC in diagnostic procedures (such as diagnosing the presence of psoriasis or
CC the propensity to develop psoriasis) and for suppressing the expression
CC of CAN-1 or STG gene (e.g. antisense inhibition, gene therapy).
CC Antibodies, raised against the polypeptides, are useful for decreasing
CC the level of CAN-1, STG or SEEK-1 biological activity in a cell. The
CC sequence presented is the human candidate coding sequence-1 (CAN-1) cDNA
XX

Sequence 891 BP; 169 A; 339 C; 196 G; 187 T; 0 U; 0 Other;
SQ

Alignment Scores:	
Pred. No.:	2.96e-24
Score:	692.00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	100.00%
BB:	6
Gaps:	0
Length:	891
Matches:	114
Conservative:	0
Mismatches:	0
Indels:	0
Gaps:	0

US-09-994-365-3 (1-114) X ABK86962 (1-891)

Dy
Dz

1 SerGluGlyHisProSerHisProProAlaGluAspArgGluGluAlaGlySerProThr 20
130 AGCGAGGGCCACCCCTTCAACCACCCGCAGAGAACGAGAGGCGCAGGCTCCCCACA 189

QY 21 LeuProGlnGlyProProValProGlyAspProTrpProGlyAlaProProLeuPheGlu 40
 |||||
 Db 190 TTGCTCAGGGCCCCCAGTCCCGGTGACCTTTGGCAGGGGACACCCCTCTTTTAA 249
 |||||

DQ 41 AspProP^{ro}P^{ro}ThrArgProSerArgProTrpArgAspLeuProGluThrGlyValTrp 60
DB 250 GATCCTCCGGCTACCGGCCAGTCGTCCCTGGAGAGAACCTGCCTGAACACTGCAATCTGG 309

QY	61	ProProGluLPProProArgThrAspProProGlnProProArgProAspAspProTPro	80
Db	310	CCCCCTGAACCGCTGAAGACGATCCTCTCAACGTC	CCCCGGCTGACGACCCCTTTGGCG 369
QY	81	AlaGlyProGlnProProGluAsnProTrrProProAlaAProGluValAspAsnAArgPro	100
Db	370	GCAGAACCCCAACCCCCACAAACCCCTGGCTCTCTGGCCCCCTGAGGTGGACACCGA	CCT 429
QY	101	GlnGlnGluProAspLeuAspProProArgGlnGluTyrArg	114
Db	430	CAGGAGGAGCCAGACTGACCCACCCCGGGAGAGGTACAGA	471

RESULT 2
ABN60006
ID ABN60006 standard; cDNA; 1473 BP

AC	ABN600006;
XX	
DT	28-JUN-2002 (first entry)
XX	

DE Novel human coding sequence SEQ ID NO: 417.

KW Human; anti-nauseatic; vulnerary; anti-inflammatory; immunomodulator;
KW antifertility; ceratoprotective; cytosolatic; rheumatic; gene therapy/
KW neuroprotective; antiparaprotection; protein therapy; EST;
KW expressed sequence tag; gene; ss.

OS Homo sapiens.

PN WO200222660-A2.

PD 21-MAR-2002

PF 10-SEP-2001; 2001WO-US026015.

PR 11-SEP-2000; 2000US-00659671.

PA (HYSE-) HYSEQ INC.

PI Tang YT, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA, Ren F;

XX

DR P-PSDB; ABB97593.

PT An isolated polynucleotide for treating diseases associated with its

XX

XX

CC novel human proteins. These were isolated from expressed sequences tags

CC haematopoiesis e.g. to treat aplastic anaemia, to help tissue regrowth

multiple sclerosis, to regulate activin or inhibin e.g. to treat

CC and cancer, to screen for drugs, to treat inflammatory conditions e.g.

CC Parkinson's disease. The present sequence is a coding sequence of the

32

Alignment Scores:

Pred. No.:	4,362-24	Length:	1
Score:	692.00	Matches:	1
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
GB:	6	Gaps:	0

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US-09-994-365-3 (1-114) x ABN6006 (1-1473)
QY 1 SerGluLysHisProSerHisProProAlaGluAspArgGluAlaGlySerProThr 20
Db AGCAGAGGACCCCTCTCAACCCGACAGAGACGAGAGGAGGAGGAGGCTCCCCAACA 761
QY 21 LeuProGlnGlyProProValProGlyAspProTrpProGlyAlaProLeuPheGlu 40
Db 762 TTGGCTCAGGGCCCCCAGTCCCGGTGACCTTGGCCAGGGGAGCCCCCTCTTTGAA 821
QY 41 AspProProProThrArgProSerArgProTrpArgAspLeuProGluThrGlyValTrp 60
Db 822 GATCCTCCGCTCAACCCGCGCCAGTGTCTCCGAGAGACCTGCTGAACTGAGTCTGG 881
QY 61 ProProGluProProAlaGlyThrAspProProGluProProAlaGProAspAspProTrpPro 80
Db 882 CCCCCTAACCCTAGAACGATCTCTCAACCTCCCGCTGACGACCTTGGGCGG 941
QY 81 AlaGlyProGlnProProGluAsnProTrpProProAlaProGluValAspAsnArgPro 100
Db 942 GCAGAGACCCAGCCCCCAGAAAAACCTCTGCTCTGCCCCCTGAGTGGACACCGACT 1001
QY 101 GlnGluGluProAspLeuAspProProArgGluGluTrpArg 114
Db 1002 CAGGAGAGCCAGACTAGACCCACCCGGGAGAGATACAGA 1043

RESULT 3
ABK6967
ID ABK6967 standard; DNA; 2997 BP.
XX ABK6967;
XX
DT 24-SEP-2002 (first entry)
XX
DE Human CAN-1 deletion polymorphism genomic DNA.
XX
XX Human; antipsoriatic; chromosome 6; candidate coding sequence-1; CAN-1;
XX SEEK-1; STG; human leukocyte antigen C; HLA C; HLA Cw6; psoriasis; skin;
XX keratinocyte; chronic inflammatory dermatosis; erythroderma; seborrheic;
XX guttate; pustular variant; Reiter's disease; hyperproliferation;
XX epidermis; differential diagnosis; gene therapy; gene; ds; SNP;
XX single nucleotide polymorphism; deletion polymorphism.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT variation replace(11..12,CCAGA)
FT /tag= a
FT /note= "Deletion polymorphism"
FT replace(114,T)
FT /tag= b
FT /standard_name= "Single nucleotide polymorphism"
FT replace(361,A)
FT /tag= c
FT /standard_name= "Single nucleotide polymorphism"
FT replace(550,A)
FT /tag= d
FT /standard_name= "Single nucleotide polymorphism"
FT replace(966,G)
FT /tag= e
FT /standard_name= "Single nucleotide polymorphism"
FT variation replace(1096,T)
FT /tag= f
FT /standard_name= "Single nucleotide polymorphism"
FT variation replace(1196,A)
FT /tag= g
FT /standard_name= "Single nucleotide polymorphism"
FT variation replace(1390,T)
FT /tag= h
FT /standard_name= "Single nucleotide polymorphism"
FT variation replace(1481..2557
FT /tag= i
FT /product= "CAN-1"

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FT exon 1481..1535
FT /tag= j
FT /number= 1
FT intron 1536..2201
FT /tag= k
FT /number= 1
FT variation replace(1677,A)
FT /tag= l
FT /standard_name= "Single nucleotide polymorphism"
FT replace(1875,T)
FT /tag= m
FT /standard_name= "Single nucleotide polymorphism"
FT variation replace(1982,A)
FT /tag= n
FT /standard_name= "Single nucleotide polymorphism"
FT variation replace(2016,C)
FT /tag= o
FT /standard_name= "Single nucleotide polymorphism"
FT variation replace(2107,G)
FT /tag= p
FT /standard_name= "Single nucleotide polymorphism"
FT exon 2202..2557
FT /tag= q
FT /number= 2
FT variation replace(2393,T)
FT /tag= r
FT /standard_name= "Single nucleotide polymorphism"
FT variation replace(2651,G)
FT /tag= s
FT /standard_name= "Single nucleotide polymorphism"
FT variation replace(2818,G)
FT /tag= t
FT /standard_name= "Single nucleotide polymorphism"
FT variation replace(2871,C)
FT /tag= u
FT /standard_name= "Single nucleotide polymorphism"
XX
XX MO20024375-A2.
XX
XX 06-JUN-2002.
XX
XX 27-NOV-2001; 2001WO-US044506.
XX
XX 28-NOV-2000; 2000US-0253592P.
XX 15-DEC-2000; 2000US-0256839P.
XX
XX (CELL-) CELTTECH R & D INC.
XX
XX Charney P, Moes P, Mceuen M;
XX WPI; 2002-508513/54.
XX P-PSDB; AAU79579.
XX
XX Novel isolated CAN-1 polypeptide involved in keratinocyte proliferation
XX and differentiation, and polynucleotides encoding the polypeptide, useful
XX for diagnosing or predicting susceptibility to psoriasis in individual.
XX
XX Example 3; Page 92-93; 95pp; English.
XX
XX The invention discloses isolated candidate coding sequence-1 (CAN-1),
XX SEEK-1 (not defined) and STG (not defined) polypeptides, and the
XX polynucleotides encoding them. All three genes were identified due to
XX their proximity to the human leukocyte antigen C (HLA C) locus on
XX chromosome 6. The HLA Cw6 allele is associated with psoriasis and as the
XX three genes are expressed in normal skin and/or keratinocyte tissue, they
XX may also have a role in psoriasis. Psoriasis is a chronic inflammatory
XX dermatosis that is characterised by hyperproliferation of epidermal
XX cells. Possible treatments against psoriasis involve the inhibition of
XX movement of cells into the epidermis, or the inhibition of
XX hyperproliferation or abnormal differentiation of keratinocytes, by the
XX inhibition of the CAN-1, STG or SEEK-1 polypeptides binding to their
XX binding partners. The polypeptides are useful for diagnosing or
XX predicting the susceptibility to psoriasis in an individual, for

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CC ameliorating the symptoms and/or progression of psoriasis and for
CC identifying agents useful for treating psoriasis or modulating the
CC activity of the polypeptide. The polypeptides are also useful for
CC enhancing the level of CAN-1, STG or SEER-1 biological activity in a cell
CC or tissue. The nucleic acid molecules are useful as hybridisation probes
CC in diagnostic procedures (such as diagnosing the presence of psoriasis or
CC the propensity to develop psoriasis) and for suppressing the expression
CC of CAN-1 or STG gene (e.g. antisense inhibition, gene therapy).
CC Antibodies, raised against the polypeptides, are useful for decreasing
CC the level of CAN-1, STG or SEER-1 biological activity in a cell. The
CC sequence presented is the human candidate coding sequence-1 (CAN-1)
CC deletion polymorphism genomic DNA
XX
SQ Sequence 2997 BP; 617 A; 785 C; 913 G; 682 T; 0 U; 0 Other;
XX
Alignment Scores:
Pred. No.: 7.53e-24 Length: 2997
Score: 692.00 Matches: 114
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-09-994-365-3 (1-114) x ABR6967 (1-2997)
QY 1 SerGluGlyHisProSerHisProProAlaGluAspArgGluGluAlaGlySerProThr 20
Db 2213 AGCGAGGGCCACCCCTTCACCCACCGCAGAGGACGAGGAGGAGGCTCCCAACA 2272
QY 21 LeuProGluGlyProProValProGluAspProTrpProGluAlaProProLeuPheGlu 40
Db 2273 TTGGCTCAGGGGCCCCCGAGTCCCGGTGACCTTGGCGAGGGGACCCCTCTTTGAA 2332
QY 41 AspProProProTrpArgProSerArgProTrpArgPheLeuProGluTrpGlyValTrp 60
Db 2333 GATCTCGGCTACCGCCCGACGTCGTCCTGGAGAGACCTGCTGAACTGGAGTCTGG 2392
QY 61 ProProGluProProArgTrpHisPheProGluProProArgProAspAspProTrpPro 80
Db 2393 CCCCTGAAACCGCTAGAACGATCTCTCAACCTCCCGGCTGACGACCTTGGCCG 2452
QY 81 AlaGlyProGluProGluAspProTrpProProAlaProGluValAspAspArgPro 100
Db 2453 GCAGGAGCCCAAGCCCAAGAAACCCCTGCGCTCTCTCCCTGAGTGGACAAACCGACT 2512
QY 101 GlnGluGluProAspLeuAspProProArgGluGluTrpArg 114
Db 2513 CAGGAGGAGCCAGACCTAGAACCCACCCCGGGAAGATACAGA 2554
RESULT 4
ABR6963 standard; DNA; 3001 BP.
XX
AC ABR6963;
XX
DT 24-SEP-2002 (first entry)
XX
DE Human candidate coding sequence-1 (CAN-1) genomic DNA.
XX
XX Human; antipsoriatic; chromosome 6; candidate coding sequence-1; CAN-1;
XX SEER-1; STG; human leukocyte antigen C; HLA C; HLA Cw6; psoriasis; skin;
XX keratinocyte; chronic inflammatory dermatosis; erythroderma; seborrheic;
XX guttate; pustular variant; Reiter's disease; hyperproliferation;
XX epidermis; differentiation; diagnosis; gene therapy; gene; ds; SNP;
XX single nucleotide polymorphism; deletion polymorphism.
XX
XX Homo sapiens.
XX
XX Key location/Qualifiers
XX variation replace(11..16,CA)
XX FT /tag= a
XX FT /note= "Deletion polymorphism"
XX FT variation replace(118,T)

FT FT /*tag= b
FT FT /standard name= "Single nucleotide polymorphism"
FT FT replace(554,A)
FT FT /*tag= c
FT FT /standard name= "Single nucleotide polymorphism"
FT FT replace(1100,T)
FT FT /*tag= d
FT FT /standard name= "Single nucleotide polymorphism"
FT FT replace(1200,A)
FT FT /*tag= e
FT FT /standard name= "Single nucleotide polymorphism"
FT FT replace(1394,T)
FT FT /*tag= f
FT FT /standard name= "Single nucleotide polymorphism"
FT FT 1485..2561
FT FT /*tag= g
FT FT /product= "CAN-1"
FT FT 1485..1539
FT FT /*tag= h
FT FT /number= 1
FT FT 1540..2205
FT FT /*tag= i
FT FT /number= 1
FT FT replace(1681,A)
FT FT /*tag= j
FT FT /standard name= "Single nucleotide polymorphism"
FT FT replace(1879,T)
FT FT /*tag= k
FT FT /standard name= "Single nucleotide polymorphism"
FT FT replace(1986,A)
FT FT /*tag= l
FT FT /standard name= "Single nucleotide polymorphism"
FT FT replace(2020,C)
FT FT /*tag= m
FT FT /standard name= "Single nucleotide polymorphism"
FT FT replace(2111,G)
FT FT /*tag= n
FT FT /standard name= "Single nucleotide polymorphism"
FT FT 2206..2561
FT FT /*tag= o
FT FT /number= 2
FT FT replace(2397,T)
FT FT /*tag= p
FT FT /standard name= "Single nucleotide polymorphism"
FT FT replace(2655,G)
FT FT /*tag= q
FT FT /standard name= "Single nucleotide polymorphism"
FT FT replace(2822,G)
FT FT /*tag= r
FT FT /standard name= "Single nucleotide polymorphism"
FT FT replace(2875,C)
FT FT /*tag= s
FT FT /standard name= "Single nucleotide polymorphism"
XX
XX WO200244375-A2.
XX
XX 06-JUN-2002.
XX
XX 27-NOV-2001; 2001WO-US044506.
XX
XX PF 28-NOV-2000; 2000US-0253592P.
XX PR 15-DEC-2000; 2000US-0256839P.
XX
XX (CELL-) CELLTECH R & D INC.
XX
XX Charmley P, Moss P, Meeuën M;
XX
XX MPI, 2002-508513/54.
XX DR P-PSDB; AAU79579.
XX
XX Novel isolated CAN-1 polypeptide involved in keratinocyte proliferation
XX and differentiation, and polynucleotides encoding the polypeptide, useful
XX for diagnosing or predicting susceptibility to psoriasis in individual.

XX Claim 18, Page 82-84; 95pp; English.

CC The invention discloses isolated candidate coding sequence-1 (CAN-1),
 CC SBEK-1 (not defined) and STG (not defined) polypeptides, and the
 CC polynucleotides encoding them. All three genes were identified due to
 CC their proximity to the human leukocyte antigen C (HLA C) locus on
 CC chromosome 6. The HLA Cw6 allele is associated with psoriasis and as the
 CC three genes are expressed in normal skin and/or keratinocyte tissue, they
 CC may also have a role in psoriasis. Psoriasis is a chronic inflammatory
 CC dermatosis that is characterised by hyperproliferation of epidermal
 CC cells. Possible treatments against psoriasis involve the inhibition of
 CC movement of cells into the epidermis, or the inhibition of
 CC hyperproliferation or abnormal differentiation of keratinocytes, by the
 CC inhibition of the CAN-1, STG or SBEK-1 polypeptides binding to their
 CC binding partners. The polypeptides are useful for diagnosing or
 CC predicting the susceptibility to psoriasis in an individual, for
 CC ameliorating the symptoms and/or progression of psoriasis and for
 CC identifying agents useful for treating psoriasis or modulating the
 CC activity of the polypeptide. The polypeptides are also useful for
 CC enhancing the level of CAN-1, STG or SBEK-1 biological activity in a cell
 CC or tissue. The nucleic acid molecules are useful as hybridisation probes
 CC in diagnostic procedures (such as diagnosing the presence of psoriasis or
 CC the propensity to develop psoriasis) and for suppressing the expression
 CC of CAN-1 or STG gene (e.g. antisense inhibition, gene therapy).
 CC Antibodies, raised against the polypeptides, are useful for decreasing
 CC the level of CAN-1, STG or SBEK-1 biological activity in a cell. The
 CC sequence presented is the human candidate coding sequence-1 (CAN-1)
 CC genomic DNA

XX Sequence 3001 BP; 619 A; 786 C; 914 G; 682 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	7 54e-24	Length:	3001
Score:	692.00	Matches:	114
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	6	Gaps:	0

US-09-994-365-3 (1-114) x ABK6963 (1-3001)

QY 1 SerGluGlyHisProSerHisProProAlaGluAspArgGluGluAlaGlySerProThr 20
 DB 2217 AGGAGGGGCCACCCCTCTCAACCCGAGAGGACGAGAGGAGGAGGCTCCACACA 2276
 QY 21 LeuProGlnGlyProProValProGlyAspProTyrProGlyAlaProProLeuPheGlu 40
 DB 2277 TTGCTCAGGGGCCGCCAGTCCCGGTGACCTTGCGCCAGGGGCAACCCCTCTTGA 2336
 QY 41 AspProProThrArgProSerArgProTyrArgAspLeuProGluTyrGluValTyr 60
 DB 2337 GATCTCTGGCTACCCGCCAGTGGTCCCTGAGAGACCTGCTGAACCTGAGAGTCTGG 2396
 QY 61 ProProGluProProArgThrAspProProGlnProProArgProAspAspProTyrPro 80
 DB 2397 CCCCTGAAACGGCTGAGAGGATCTCTCAACCTCCCGGCTGACGACCTTGGCCG 2456
 QY 81 AlaGlyProGlnProProGluAsnProTyrProProAlaProGluValAspAsnArgPro 100
 DB 2457 GCGAGACCCCGAGCCCGCAAAACCCCTGCTCTCCCTGAGGTGAGCAACCGACCT 2516
 QY 101 GlnGluGluProAspLeuAspProProArgGluGluTyrArg 114
 DB 2517 CAGGAGGAGCAAGCCTAGACCAACCCGGGAAAGATACAGA 2558

RESULT 5

AAH45310
 ID AAH45310 standard; DNA; 25235 BP.
 AC AAH45310;
 XX
 DT 01-OCT-2001 (first entry)

XX Human SBEK1 DNA.

XX Human, MHC S; major histocompatibility complex S; vulgar psoriasis;
 KW diagnosis; primer; SBEK1; HCR; a-helix coiled-coil rod homologue;
 XX polymorphism; ds.
 OS Homo sapiens.

Key	Location/Qualifiers
FT exon	1..420
FT intron	/*tag= a
FT exon	421..1281
FT exon	/*tag= b
FT exon	1282..1405
FT intron	/*tag= c
FT intron	1406..1601
FT exon	/*tag= d
FT exon	1602..1702
FT intron	/*tag= e
FT intron	1703..2351
FT exon	/*tag= f
FT exon	2352..2364
FT intron	/*tag= g
FT intron	2365..6286
FT exon	/*tag= h
FT exon	6287..6509
FT intron	/*tag= i
FT intron	6510..10416
FT exon	/*tag= j
FT exon	10417..10493
FT exon	/*tag= k
FT intron	10494..14243
FT exon	/*tag= l
FT exon	14244..14407
FT intron	/*tag= m
FT intron	14408..14243
FT exon	/*tag= n
FT exon	25190..25235
FT exon	/*tag= o

XX WO200142458-A1.

XX 14-JUN-2001.

XX 06-DEC-2000; 2000MOJUP008624.

XX 06-DEC-1999; 99JP-00346867.

XX (INOK/) INOKO H.

XX Inoko H, Tamiya G;

XX WPI; 2001-381680/40.

XX New primer DNA, useful for detecting vulgar psoriasis.

XX Claim 1; Page 46-62; 106pp; Japanese.

XX The invention relates to a method of diagnosing vulgar psoriasis using
 CC primers based on the sequences of the human MHC S, SBEK1 and HCR genes.
 CC By analysing the sequences of these genes in Japanese patients with
 CC psoriasis and in normal subjects, it has been found that some of the
 CC examined polymorphisms correlate significantly to the group of patients
 CC with psoriasis. Vulgar psoriasis can therefore be diagnosed by analysing
 CC these gene polymorphisms. The present sequence is the human SBEK1 gene
 CC which was used to design primers for use in the invention

XX Sequence 25235 BP; 5967 A; 6703 C; 6487 G; 6078 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 3..89e-23 Length: 25235
 Score: 692.00 Matches: 114

Percent Similarity: 100.00%
 Best Local Similarity: 100.00%
 Query Match: 100.00%
 DB: 4
 Gaps: 0

Conservative: 0
 Mismatches: 0
 Indels: 0
 Gaps: 0

US-09-994-365-3 (1-114) x AAH45310 (1-25235)

QY 1 SerGluGlyHisProSerHisProProAlaGluAspArgGluGluAlaGlySerProThr 20
 DB 1766 AGCAGAGGCGCACCCCTCTCAACCCGACAGAGAGCGAGGAGGCTCCCAACA 1825
 QY 21 LeuProGluGlyProProValProGlyAspProThrProGlyAlaProProLeuPheGlu 40
 DB 1826 TTGCTCAAGGAGCCGCCAGTCCCGGTGACCTTGCGCAGGAGCAACCCCTCTTTGAA 1885
 QY 41 AspProProProThrArgProSerArgProThrArgAspLeuProGluThrGlyValTyr 60
 DB 1886 GATCTCCGCTTACCCGCGCCAGTCTCTGAGAGACCTGCTGAACTGGAGTCTGG 1945
 QY 61 ProProGluProProArgThrAspProProGluProProArgProAspAspProTyrPro 80
 DB 1946 CCCCTGAAACCGCTAGACGATCTCTCAACCTCCCGGCTGACGACCTTTGGCCG 2005
 QY 81 AlaGlyProGluProProGluAspProThrProProAlaProGluValAspAsnArgPro 100
 DB 2006 GCAGAGACCCGACCCCAAGAAACCCCTGCTCTCCCTGAGGTGACAAACGACCT 2065
 QY 101 GlnGluGluProAspLeuAspProProArgGluGluTyrArg 114
 DB 2066 CAGAGAGAGCCAGACCTAGACCCCGGGAAGATACAGA 2107
 RESULT 6
 ABQ75680 standard; DNA; 55050 BP.
 XX ABQ75680;
 AC
 XX
 DT 11-NOV-2002 (first entry)
 XX
 DE Human SEEK1 consensus genomic DNA.
 XX
 KM Human; SEEK1; chromosome 6p21; inflammatory disease; antiinflammatory;
 KW antiporiatic; gene therapy; gene; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200264831-A2.
 PD 22-AUG-2002.
 PF 13-FEB-2002; 2002WO-GB000653.
 PR 13-FEB-2001; 2001GB-00003514.
 XX
 PA (OXAG-) OXAGEN LTD.
 XX
 PI Lench NJ, Allen MJ, Nicholls RK;
 XX
 DR WPI; 2002-667013/71.
 XX
 PT Polymorphisms in the SEEK1 gene and polymucleotides encoding the SEEK1
 PT gene, for treating, diagnosing or determining susceptibility to SEEK1
 PT mediated disease, e.g. inflammatory disease such as psoriasis.
 XX
 PS Claim 4; Fig 2; 69pp; English.
 XX
 CC The present invention describes a polymucleotide (I) comprising: (a) a
 CC nucleic acid sequence (II) encoding the SEEK1 gene; (b) a nucleic acid
 CC sequence (III) encoding a fragment of the SEEK1 gene; or (c) a nucleic
 CC acid sequence (IV) that hybridises under stringent conditions to a nucleic
 CC polymucleotide of (II) or (III). (I) has antiinflammatory and
 CC antipsoriatic activities and can be used in gene therapy. The alleles of
 CC one or more polymorphisms in the SEEK1 gene can be used for the

CC manufacture of a medicament for the diagnosis and treatment of SEEK1
 CC mediated disease. SEEK1 protein fragments are useful in diagnostic,
 CC prognostic or therapeutic methods, or as research tools in drug
 CC screening. Human SEEK1 is located to chromosome 6p21. The present
 CC sequence represents a human SEEK1 nucleotide sequence
 XX

SQ Sequence 55050 BP; 13076 A; 14198 C; 14560 G; 13197 T; 0 U; 19 Other;

Alignment Scores:

Pred. No.: 7, 11e-23 Length: 55050

Score: 692.00 Matches: 114

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 6 Gaps: 0

US-09-994-365-3 (1-114) x ABQ75680 (1-55050)

QY 1 SerGluGlyHisProSerHisProProAlaGluAspArgGluGluAlaGlySerProThr 20

DB 27111 AGCAGAGGCGCACCCCTCTCAACCCGACAGAGAGCGAGAGGAGGCTCCCAACA 27170

QY 21 LeuProGluGlyProProValProGlyAspProThrProGlyAlaProProLeuPheGlu 40

DB 27171 TTGCTCAAGGAGCCGCCAGTCCCGGTGACCTTGCGCAGGAGCAACCCCTCTTTGAA 27230

QY 41 AspProProProThrArgProSerArgProThrArgAspLeuProGluThrGlyValTyr 60

DB 27231 GATCTCCGCTTACCCGCGCCAGTCTCTGAGAGACCTGCTGAACTGGAGTCTGG 27290

QY 61 ProProGluProProArgThrAspProProGluProProArgProAspAspProTyrPro 80

DB 27291 CCCCTGAAACCGCTAGACGATCTCTCAACCTCCCGGCTGACGACCTTTGGCCG 27350

QY 81 AlaGlyProGluProProGluAspProThrProProAlaProGluValAspAsnArgPro 100

DB 27351 GCAGAGACCCGACCCCAAGAAACCCCTGCTCTCCCTGAGGTGACAAACGACCT 27410

QY 101 GlnGluGluProAspLeuAspProProArgGluGluTyrArg 114

DB 27411 CAGAGAGAGCCAGACCTAGACCCCGGGAAGATACAGA 27452

RESULT 7

ACH72505 standard; DNA; 565 BP.

XX ACH72505;
 AC
 XX
 DT 29-UTL-2004 (first entry)
 XX
 DE Human genome derived single exon probe #5700.
 XX
 KM Human; probe; ss; gene expression; single exon probe; microarray;
 KW alternative splicing event; genomic alteration.
 XX
 OS Homo sapiens.
 XX
 PN US2003194704-A1.
 PD 16-OCT-2003.
 PF 03-APR-2002; 2002US-00029386.
 PR 03-APR-2002; 2002US-00029386.
 XX
 PA (PENK/) PENK S G.
 PA (RANK/) RANK D R.
 PA (HANZ/) HANZEL D K.
 PI Penn SG, Rank DR, Hanzel DK;
 XX
 DR WPI; 2004-119264/12.
 XX

PT New human genome-derived single exon nucleic acid probes useful for human
PT gene expression analysis, for identifying or characterizing alternative
PT splicing events, for assessing genomic alterations or as tools for
PT surveying tissues.

PS Claim 15; SEQ ID NO 5700; 80pp; English.

XX The invention relates to a nucleic acid probe for measuring human gene
XX expression, comprising any of the 27,400 fully defined nucleotide
XX sequences in the specification, or their complements or fragments, and
XX encoding at least 8 amino acids of any of the 6888 amino acid sequences
XX fully defined in the specification. The probe is a single exon probe that
XX hybridizes under high stringency conditions to a nucleic acid molecule
XX expressed in human cells or tissues. Also included are a spatially-
XX addressable set of single exon nucleic acid probes for measuring human
XX gene expression (comprising a plurality of single exon nucleic acid
XX probes cited above, where each of the plurality of probes is separately
XX and addressably isolatable or amplifiable from the plurality), a single
XX exon microarray for measuring human gene expression, a method of
XX measuring human gene expression, a vector comprising the single exon
XX probe cited above, an ORF-encoded peptide comprising at least 8
XX contiguous amino acids of any of the above-mentioned amino acid
XX sequences (optionally with conservative amino acid substitutions), an
XX isolated antibody that binds specifically to a peptide cited above,
XX methods of selling and/or licensing single exon probes or microarrays to
XX a customer desiring to measure gene expression, a method of providing
XX human gene expression data by subscription, and a computer-readable
XX storage medium which contains a database having a plurality of records
XX (each record including data on the expression of a single exon probe
XX cited above). The probe, methods and apparatus are useful in gene
XX expression analysis. The probes may be used as tools for surveying
XX tissues to detect the presence of expressed messages that contain their
XX specific exon, or in constructing genome-derived single exon microarrays.
XX In addition, the probes are used in identifying and characterizing
XX alternative splicing events, in detecting and characterizing gross
XX alterations in the genomic locus that includes their exon, in assessing
XX smaller genomic alterations, in priming the synthesis of nucleic acids,
XX or in expressing the ORF-encoded peptide. The present sequence is a human
XX single exon probe of the invention. Note: The sequence data for this
XX patent did not form part of the printed specification, but was obtained
XX in electronic format directly from USPTO at
XX seqdata.uspto.gov/sequence.html?docID=20030194704

XX Sequence 565 BP; 99 A; 227 C; 112 G; 127 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	7.16e-15	Length:	565
Score:	486.00	Matches:	79
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	70.23%	Indels:	0
DB:	12	Gaps:	0

US-09-994-365-3 (1-114) x ACH72505 (1-565)

QY 36 ProProLeuPhaGluAspProProProThraArgProSerArgProTTPaArgAspLeuPro 55
DB 1 CCCCCTCTTTGAAAGATCCTCCGCTAACCCGCCGCGTCCCTGGAAGAGACTGCT 60
QY 56 GATTThG1ValTTPProProGluProProArgThraArgProProGluProProArgPro 75
DB 61 GAAAGCTGAGATCTGGCCCCCTGAAACCGCTGAAAGGATCTCTCAACTCCCCGGCT 120
QY 76 AspAspProTTPProAlaGlyProGluProProGluAsnProTTPProProAlaProGlu 95
DB 121 GACGACCTTGGCGCGGACGAGACCCCAAGAAACCCCTTGGCTCTCGCCCTGAG 180
QY 96 ValAspAsnArgProGlnGlnGluProAspLeuAspProProArgGluGluTTPArg 114
DB 181 GTGAGACAAACGACCTCAGAGAGAGACGACCTTACCCACCCCGGAGAGATACAGA 237

RESULT 8
ACH86315

ID ACH86315 standard; DNA; 157 BP.

XX ACH86315;

DT 29-JUL-2004 (first entry)

DE Human genome derived single exon probe #19510.

KW Human; probe; as; gene expression; single exon probe; microarray;
KW alternative splicing event; genomic alteration.

OS Homo sapiens.

PN US2003194704-A1.

PD 16-OCT-2003.

PF 03-APR-2002; 2002US-00029386.

PR 03-APR-2002; 2002US-00029386.

PA (PENN/) PENN S G.
PA (RANK/) RANK D R.
PA (HANZ/) HANZEL D K.

PI Penn SG, Rank DR, Hanzel DK,

XX WPI; 2004-119264/12.

XX WPI; 2004-119264/12.

PT New human genome-derived single exon nucleic acid probes useful for human
PT gene expression analysis, for identifying or characterizing alternative
PT splicing events, for assessing genomic alterations or as tools for
PT surveying tissues.

PS Claim 1; SEQ ID NO 19510; 80pp; English.

XX The invention relates to a nucleic acid probe for measuring human gene
XX expression, comprising any of the 27,400 fully defined nucleotide
XX sequences in the specification, or their complements or fragments, and
XX encoding at least 8 amino acids of any of the 6888 amino acid sequences
XX fully defined in the specification. The probe is a single exon probe that
XX hybridizes under high stringency conditions to a nucleic acid molecule
XX expressed in human cells or tissues. Also included are a spatially-
XX addressable set of single exon nucleic acid probes for measuring human
XX gene expression (comprising a plurality of single exon nucleic acid
XX probes cited above, where each of the plurality of probes is separately
XX and addressably isolatable or amplifiable from the plurality), a single
XX exon microarray for measuring human gene expression, a method of
XX measuring human gene expression, a vector comprising the single exon
XX probe cited above, an ORF-encoded peptide comprising at least 8
XX contiguous amino acids of any of the above-mentioned amino acid
XX sequences (optionally with conservative amino acid substitutions), an
XX isolated antibody that binds specifically to a peptide cited above,
XX methods of selling and/or licensing single exon probes or microarrays to
XX a customer desiring to measure gene expression, a method of providing
XX human gene expression data by subscription, and a computer-readable
XX storage medium which contains a database having a plurality of records
XX (each record including data on the expression of a single exon probe
XX cited above). The probe, methods and apparatus are useful in gene
XX expression analysis. The probes may be used as tools for surveying
XX tissues to detect the presence of expressed messages that contain their
XX specific exon, or in constructing genome-derived single exon microarrays.
XX In addition, the probes are used in identifying and characterizing
XX alternative splicing events, in detecting and characterizing gross
XX alterations in the genomic locus that includes their exon, in assessing
XX smaller genomic alterations, in priming the synthesis of nucleic acids,
XX or in expressing the ORF-encoded peptide. The present sequence is a human
XX single exon probe of the invention. Note: The sequence data for this
XX patent did not form part of the printed specification, but was obtained
XX in electronic format directly from USPTO at
XX seqdata.uspto.gov/sequence.html?docID=20030194704

XX Sequence 157 BP; 38 A; 64 C; 38 G; 17 T; 0 U; 0 Other;

[illegible][illegible]

Qy 83 -----ProGlnProGluAsnProTrrProGAlaProGluValaAspAsnArg 99
 Db 91065 CCGGAGCCCCCAAGTCCGCCGGAGCCACCCTGCGCGCGGACACCGCTTG----- 91015
 Qy 100 ProGlnGluGluProAspLeuAspPro 108
 Db 91014 CCGAATAGCAGCCCGCGCTTGCCGCCG 90988

RESULT 13
 AAI23276/C
 ID AAI23276 standard; DNA; 446 BP.
 XX
 AC AAI23276;
 XX
 DT 12-OCT-2001 (first entry)
 XX
 DE Probe #13209 for gene expression analysis in human cervical cell sample.
 XX
 KW Probe; human; microarray; gene expression; cervical epithelial cell;
 KM cervical cancer; ss.
 XX
 OS Homo sapiens.
 XX
 PN MO200157278-A2.
 XX
 PD 09-AUG-2001.
 XX
 PF 30-JAN-2001; 2001WO-US000670.
 XX
 PR 04-FEB-2000; 2000US-0180312P.
 XX
 PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00608408.
 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 XX
 XX (MOLE-) MOLECULAR DYNAMICS INC.
 PA Penn SG, Hanzel DK, Chen W, Rank DR;
 PI WPI; 2001-488901/53.
 DR
 XX
 PT Human genome-derived single exon nucleic acid probes useful for analyzing
 PT gene expression in human cervical epithelial cells.
 XX
 PS Claim 25; SEQ ID NO 13209; 487bp; English.
 XX
 CC The present invention relates to human single exon nucleic acid probes
 CC (SENPs). The present sequence is one such probe. The SENPs are derived
 CC from human HeLa cells. The SENPs can be used to produce a single exon
 CC microarray, which can be used for measuring human gene expression in a
 CC sample derived from human cervical epithelial cells. By measuring gene
 CC expression, the probes are therefore useful in grading and/or staging of
 CC diseases of the cervix, notably cervical cancer. Note: The sequence data
 CC for this patent did not form part of the printed specification, but was
 CC obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 446 BP; 31 A; 26 C; 254 G; 135 T; 0 U; 0 Other;
 XX

Alignment Scores:
 Pred. No.: 0.285 Length: 446
 Score: 190.50 Matches: 43
 Percent Similarity: 40.00% Conservative: 1
 Best Local Similarity: 39.09% Mismatches: 57
 Query Match: 27.53% Indels: 9
 DB: 4 Gaps: 2

US-09-994-365-3 (1-114) x AAI23276 (1-446)
 Qy 5 ProSerHisProAlaGluAspArgGluGluAlaGlySerProThrLeuProGlnGly 24

Db 403 CCACCAACCAACCAACCAATCAACCAACCAACCAACCAATCAACCAACCAATCA 344
 Qy 25 ProProValProGlyAspProTrrProGlyAlaProProLeuPheGluAspProPro 44
 Db 343 CCACCAACCAACCAATCAACCAACCAACCAACCAACCAACCAATCAACCAACCA 284
 Qy 45 ThrArgProSerArgProTrrArgAspLeuProGluThrGlyValTrrProGluPro 64
 Db 283 CCACCAACCAATCAACCAACCAATCAATCAACCA-----CCACCAACCA 236
 Qy 65 ProArgThrAspProProGlnProProArgProAspAspProTrrProAlaGlyProGln 84
 Db 235 CCACCAATCAACCAACCAACCAACCAACCAATCAACCAACCAACCAATCAATCA 176
 Qy 85 ProProGluAsnProTrrPro-----ProAlaProGluValaAspAsnArg 99
 Db 175 CCACCAACCAACCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCA 116
 Qy 100 ProGlnGluGluProAspLeuAspProPro 109
 Db 115 CCGCGCGCACCAACCGCGCATGCGCACCGCCA 86

RESULT 14
 ABA68382/C
 ID ABA68382 standard; DNA; 446 BP.
 XX
 AC ABA68382;
 XX
 DT 01-FEB-2002 (first entry)
 XX
 DE Human foetal liver single exon nucleic acid probe #16687.
 XX
 KW Human; foetal liver; gene expression; single exon nucleic acid probe; ss.
 OS Homo sapiens.
 XX
 PN WO200157277-A2.
 XX
 PD 09-AUG-2001.
 XX
 PF 30-JAN-2001; 2001WO-US000669.
 XX
 PR 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00608408.
 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 XX
 XX (MOLE-) MOLECULAR DYNAMICS INC.
 PA Penn SG, Hanzel DK, Chen W, Rank DR;
 PI WPI; 2001-483447/52.
 DR
 XX
 PT Human genome-derived single exon nucleic acid probes useful for analyzing
 PT gene expression in human foetal liver.
 XX
 PS Claim 4; SEQ ID NO 16687; 639bp + Sequence Listing; English.
 XX
 CC The invention relates to a single exon nucleic acid probe for measuring
 CC human gene expression in a sample derived from human foetal liver. The
 CC single exon nucleic acid probes may be used for predicting, measuring and
 CC displaying gene expression in samples derived from human foetal liver. The
 CC present sequence is a single exon nucleic acid probe of the invention.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 446 BP; 31 A; 26 C; 254 G; 135 T; 0 U; 0 Other;
 XX

Alignment Scores:
 Pred. No.: 0.285 Length: 446
 Score: 190.50 Matches: 43
 Percent Similarity: 40.00% Conservative: 1
 Best Local Similarity: 39.09% Mismatches: 57
 Query Match: 27.53% Indels: 9
 DB: 4 Gaps: 2

Pred. No.:	0.285	Length:	446
Score:	190.50	Matches:	43
Percent Similarity:	40.00%	Conservative:	1
Best Local Similarity:	39.09%	Mismatches:	57
Query Match:	27.53%	Indels:	3
DB:	4	Gaps:	2

US-09-994-365-3 (1-114) x ABA68382 (1-446)

[illegible]

RESULT 15
AAI48596/c
ID AAI48596 standard; DNA; 446 BP.

AC AA148596 ;

DT 17-OCT-2001 (first entry)

Probe #17282 used to measure gene expression in human placenta sample.

Probe; microarray; human; placenta; antenatal diagnosis;
genetic disorder; ss.

OS Homo sapiens.

PN WQ200157272-A2.

PD 09-AUG-2001

PF 30-JAN-2001; 2001WO-US000663

04-FEB-2000; 2000US-0180312P

PR	30-JUN-2000;	2000US-00608408;
DP	03-AUG-2000;	2000US-00632355;

PR 21-SEP-2000; 2000US-0234687P
 PP 27-SEP-2000; 2000US-02346359P

PR 04-OCT-2000; 2000GB-00024263
XX

PA (MOLE-) MOLECULAR DYNAMICS INC
XX

PI Penn SG, Hanzel DK, Chen W, Krank DK, XY

DR WPI; 2001-488897/53.
YY

PT Human genome-derived single exon nucleic acid probes useful for analyzing PT gene expression in human placenta.

PS Claim 25; SEQ ID NO 17282; 654pp; English

CC The present invention relates to single exon nucleic acid probes (SENPs).
 CC The present sequence is one such probe. The probes are useful for
 CC producing a microarray for predicting, measuring and displaying gene
 CC expression in samples derived from human placenta. The probes are useful
 CC for antenatal diagnosis of human genetic disorders
 XX
 XX Sequence 446 BP, 31 A, 26 C, 254 G, 135 T, 0 U, 0 Other;

Alignment Scores:

Pred. No.:	0.285	Length:	446
Score:	190.50	Matches:	43
Percent Similarity:	40.00%	Conservative:	1
Best Local Similarity:	39.09%	Mismatches:	57
Query Match:	27.53%	Indels:	
DB:	4	Gaps:	2

US-09-994-365-3 (1-114) X AA148596 (1-446)

Df

Oy		ProSerHisProProAlaIusprgrIngluIaglyserProThrleProInglyl	24
Dd	403	CCACCAACCACCATCACCATCACCACCAACCACCATCACCAACCAATCA	344
Oy	25	ProProValProGlyAspProTrrPProGlyAlaProProLeuPhagiUasProProPro	44
Dd	343	CCACCAACACCAATCACCAACCAACCAACCAACCAATCACCAACCAACCA	284
Oy	45	ThirArgProSerArgProTrrPargAspleuProGluThrGlyValTrrProProGluPro	64
Dd	283	CCACCAACCATCACCACTACCATCATCACCA-----CCACCAACCA	236
Oy	65	ProArgThrAspProProGluProProArgProAspAspProTrrPProAlaGlyProGln	84
	:::		
Dd	235	CCACCATCACCAACCAACCAACCAACCAACCAATCACCAACCAACCAATCA	176
Oy	85	ProProGluAsnProTrrPro-----ProAlaProGluValAspAsnArg	99
Dd	175	CCAACAACCAACCAATCACCATTCATCACCAACCATCACCGGCACCATCACCAACCA	116
Oy	100	ProGlnIngluIuProAspleuAspProPro	109
Dd	115	CCGCCGCCAACCCGGCACTGCCACCGCA	86

Search completed: January 11, 2005, 12:05:14
Job time : 402.064 secs

ORIGIN AGPOPENPMPAPAEVDNRPQEBPDLDPREBYR"

Alignment Scores:

Pred. No.: 5.48e-20 Length: 891
 Score: 692.00 Matches: 114
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0

US-09-994-365-3 (1-114) x AX477387 (1-891)

QY 1 SerGluGlyHisProSerHisProProAlaGluAspArgGluGluAlaGlySerProThr 20
 Db 130 AGGAGAGGCCACCCCTCTCAACCCAGAGAGACCGAGAGGAGGAGGCTCCCAACA 189
 QY 21 LeuProGlnGlyProProValProGlyAspProTyrProGlyAlaProProLeuPheGlu 40
 Db 190 TTGGCTCAGGGGCCCCCAAGTCCCGGTGACCTTGGCGACGGGCAACCCCTCTTGGAA 249
 QY 41 AspProProProThrArgProSerArgProTyrArgAspLeuProGluTyrGlyValTyr 60
 Db 250 GATCTCCGCTACCCGCCCAAGTCTGCTCGAGAGACCTGCTGAACCTGAGAGTCTGG 309
 QY 61 ProProGluProProArgTyrAspProProGlnProProArgProAspAspProTyrPro 80
 Db 310 CCCCTGAACCGCTAGACGAGATCCCTCAACCTCCCGGCTGACGACCTTGGCCG 369
 QY 81 AlaGlyProGlnProProGluAsnProTyrProProAlaProGluValAspAsnArgPro 100
 Db 370 GCAAGACCCAGCCCGCAAGAAACCCCTGCTCCCTGAGGTGACCAACCGACCT 429
 QY 101 GlnGluGluProAspLeuAspProProArgGluGluTyrArg 114
 Db 430 CAGGAGAGCCAGACCTAGACCCACCCGGAGAGATACAGA 471

RESULT 2
 LOCUS CQ722444 1143 bp DNA linear PAT 03-FEB-2004
 DEFINITION Sequence 8378 from Patent WO02068579.
 ACCESSION CQ722444
 VERSION CQ722444.1 GI:42283301
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 TITLE Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

JOURNAL
 FEATURES
 source
 1. 1143
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"
 Location/Qualifiers

ORIGIN

Alignment Scores:

Pred. No.: 6.56e-20 Length: 1143
 Score: 692.00 Matches: 114
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0

US-09-994-365-3 (1-114) x CQ722444 (1-1143)

QY 1 SerGluGlyHisProSerHisProProAlaGluAspArgGluGluAlaGlySerProThr 20

Db 382 AGGAGAGGCCACCCCTCTCAACCCAGAGACCGAGAGGAGGAGGCTCCCAACA 441

QY 21 LeuProGlnGlyProProValProGlyAspProTyrProGlyAlaProProLeuPheGlu 40
 Db 442 TTGGCTCAGGGGCCCCCAAGTCCCGGTGACCTTGGCGACGGGCAACCCCTCTTGGAA 501

QY 41 AspProProProThrArgProSerArgProTyrArgAspLeuProGluTyrGlyValTyr 60
 Db 502 GATCTCCGCTACCCGCCCAAGTCTGCTCGAGAGACCTGCTGAACCTGAGAGTCTGG 561

QY 61 ProProGluProProArgTyrAspProProGlnProProArgProAspAspProTyrPro 80
 Db 562 CCCCTGAACCGCTAGACGAGATCCCTCAACCTCCCGGCTGACGACCTTGGCCG 621

QY 81 AlaGlyProGlnProProGluAsnProTyrProProAlaProGluValAspAsnArgPro 100
 Db 622 GCAAGACCCAGCCCGCAAGAAACCCCTGCTCCCTGAGGTGACCAACCAACCT 681

QY 101 GlnGluGluProAspLeuAspProProArgGluGluTyrArg 114
 Db 682 CAGGAGAGCCAGACCTAGACCCACCCGGAGAGATACAGA 723

RESULT 3

LOCUS AB031480 1143 bp mRNA linear PRI 08-DEC-1999
 DEFINITION Homo sapiens SPRI mRNA, complete cds.
 ACCESSION AB031480
 VERSION AB031480.1 GI:6539433

KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 TITLE Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (sites)

Okazaki, Tamiya, G., Tomizawa, M., Oka, M., Katsuyama, Y., Makino, S.,
 Shihina, T., Yoshitome, M., Lizuka, M., Sasao, Y., Iwashita, K.,
 Kawakubo, Y., Sugai, J., Ozawa, A., Ohkido, M., Kimura, M., Bahram, S.
 and Inoko, H.

Association analysis using refined microsatellite markers localizes
 a susceptibility locus for psoriasis vulgaris within a 111 kb
 segment telomeric to the HLA-C gene
 Hum. Mol. Genet. 8 (12), 2165-2170 (1999)

JOURNAL
 MEDLINE 20014706
 PUBMED 10545595
 REFERENCES 2 (bases 1 to 1143).

AUTHORS Tamiya, G., Tomizawa, M., Makino, S., Oka, A., Nakajima, K., Kimura, M.
 and Inoko, H.

TITLE Direct Submision
 JOURNAL Submited (25-AUG-1999) Akira Oka, Tokai University School of
 Medicine, Division of Molecular Life Science; Bohseidai, Ishihara,
 Kanagawa 259-1193, Japan (E-mail:oka246@is.icc.u-tokai.ac.jp,
 Tel:81-463-93-1121(ex.2579), Fax:81-463-94-8884)

FEATURES
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 1. 1143
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 /mol_type="mRNA"
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 /sex="male"
 /cell_type="epidermal keratinocytes"
 1. 1143

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 CDS
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ORIGIN

Alignment Scores:

Pred. No.: 6 566-20 Length: 1143
Score: 692.00 Matches: 114
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-994-365-3 (1-114) x AB031480 (1-1143)

Qy 1 SerGluGlyHisProSerHisProProAlaGluAspArgGluGluAlaGlySerProThr 20

Db 382 AGGAGAGGCCACCCCTCTCAACCCAGAGAGACCGAGAGAGGAGGAGGCTCCCAACA 441

Qy 21 LeuProGlnGlyProProValProGlyAspProTrpProGlyValaProProlaPheGlu 40

Db 442 TTGGCTCAGAGGCCCCCAAGTCCCGGTGACCTTGGCCAGGGGCAACCCCTCTTTGAA 501

Qy 41 AspProProThrArgProSerArgProTrpArgAspLeuProGluThrGlyValaTrp 60

Db 502 GATCTCTGGCTACCCGCCAGTCTGCTGAGAGACTGCTGAACCTGAGGTCTGG 561

Qy 61 ProProGluProProArgTrpAspProProGlnProProArgProAspAspProTrpPro 80

Db 562 CCCCTTAACCGCTAGAGGATCTCTCAACCTCCGGGCTGAGAGACCTTGGCG 621

Qy 81 AlaGlyProGlnProProGluAsnProTrpProProAlaProGluValaAspAsnArgPro 100

Db 622 GCAGAGACCCAGCCGCCAGAAAACCTGGCTCTCCCTCGAGTGGACCAACCGACT 681

Qy 101 GlnGluGluProAspLeuAspProProArgGluGluTrpArg 114

Db 682 CAGAGAGCCAGACTAGACCCAGGAGAGTACAGA 723

Qy 682 CAGAGAGCCAGACTAGACCCAGGAGAGTACAGA 723

RESULT 4 AF484420 1185 bp mRNA linear PRI 02-MAR-2003

LOCUS AF484420 Homo sapiens psoriasis susceptibility 1 candidate 2 (PSORS1C2)

DEFINITION mRNA, complete cds.

ACCESSION AF484420.1 GI:28628834

VERSION AF484420.1 GI:28628834

KEYWORDS Homo sapiens (human)

SOURCE Homo sapiens

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

TITLE 1 (bases 1 to 1185)

JOURNAL Holm,S.U., O'Brien,K.P., Carlen,L. and Stahle-Backdahl,M.

AUTHORS The PSORS1C1 and PSORS1C2 genes in 6p21.3 associate strongly with

TITLE psoriasis in the Swedish population

JOURNAL Unpublished

REFERENCES 2 (bases 1 to 1185)

AUTHORS Holm,S.U., O'Brien,K.P., Carlen,L. and Stahle-Backdahl,M.

TITLE Direct Submission

JOURNAL Submitted (15-FEB-2002) Dermatology, Karolinska Institute, L8:02

FEATURES Karolinska Sjukhuset, Stockholm S-17176, Sweden

SOURCE Location/Qualifiers

1. 1185

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/chromosome="6"

/map="6p21.3"

/tissue_type="skin"

1. 1185

/gene="PSORS1C2"

325..735

/gene="PSORS1C2"

/codon_start=1

/product="psoriasis susceptibility 1 candidate 2"

/protein_id="AA049377.1"

/db_xref="GI:28628835"

ORIGIN

Alignment Scores:
Pred. No.: 6 736-20 Length: 1185
Score: 692.00 Matches: 114
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-994-365-3 (1-114) x AF484420 (1-1185)

Qy 1 SerGluGlyHisProSerHisProProAlaGluAspArgGluGluAlaGlySerProThr 20

Db 391 AGGAGAGGCCACCCCTCTCAACCCAGAGAGACCGAGAGAGGAGGAGGCTCCCAACA 450

Qy 21 LeuProGlnGlyProProValProGlyAspProTrpProGlyValaProProlaPheGlu 40

Db 451 TTGGCTCAGAGGCCCCCAAGTCCCGGTGACCTTGGCCAGGGGCAACCCCTCTTTGAA 510

Qy 41 AspProProThrArgProSerArgProTrpArgAspLeuProGluThrGlyValaTrp 60

Db 511 GATCTCTGGCTACCCGCCAGTCTGCTGAGAGACTGCTGAACCTGAGGTCTGG 570

Qy 61 ProProGluProProArgTrpAspProProGlnProProArgProAspAspProTrpPro 80

Db 571 CCCCTTAACCGCTAGAGGATCTCTCAACCTCCGGGCTGAGAGACCTTGGCG 630

Qy 81 AlaGlyProGlnProProGluAsnProTrpProProAlaProGluValaAspAsnArgPro 100

Db 631 GCAGAGACCCAGCCGCCAGAAAACCTGGCTCTCCCTCGAGTGGACCAACCGACT 690

Qy 101 GlnGluGluProAspLeuAspProProArgGluGluTrpArg 114

Db 691 CAGAGAGCCAGACTAGACCCAGGAGAGTACAGA 732

RESULT 5 AX406002 1473 bp DNA linear PAT 14-JUN-2002

LOCUS AX406002 Sequence 417 from Patent WO0222660.

DEFINITION AX406002

ACCESSION AX406002.1 GI:21439443

VERSION AX406002.1 GI:21439443

KEYWORDS Homo sapiens (human)

SOURCE Homo sapiens

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

TITLE 1 (bases 1 to 1473)

JOURNAL Tang,Y.T., Liu,C., Zhou,P., Asundi,V., Zhang,J., Zhao,Q.A., Ren,F.,

AUTHORS Xue,A.J., Yang,Y., Wehrman,T. and Dymnac,R.T.

TITLE Novel nucleic acids and polypeptides

JOURNAL Patent: WO 0222660-A 417 21-MAR-2002;

HYSBO, INC. (US)

FEATURES Location/Qualifiers

1. 1473

/organism="Homo sapiens"

/mol_type="unassigned DNA"

/db_xref="taxon:9606"

636..1046

/note="unamed protein product"

/codon_start=1

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/translaction="MILNKLGLIVLCILHTRGISGSEGHSPHPADREAGSPPLP

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ORIGIN

Alignment Scores:

Pred. No.: 7 886-20 Length: 1473

7.886-20 Length: 1473

1473

1473

1473

1473

Score:	693.00	Matches:	114
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
Gaps:	6	Gaps:	0

US-09-994-365-3 (1-114) x AX406002 (1-1473)

QY 1 SerGIuGIyhiSPoSeRhiSPoPrOlaGIuASpArGIuGIuAlGIySePrOthR 20
Db 702 AGCGAGGGCCACCCCTCTACCCACCCGCAAGACCGAGAGGAGGCGGCTCCCAACA 761

0y	21	LeuProGlnGlyProProVal.ProGlyAspProTyrProGlyAlaProProLeuPheGlu	40
Db	762	TTGCCTCAGGGCCCCCAGTCCCGGTGACCTTGGCCAGGGGACACCCCTCTTTTGA	821

4 AspProProThrArgProSerArgProTpaArgspLeuProGluThrGlyValTrp 60
822 GATCTCCGCGCTACCGCGCCAGTCTGTCTCTGGAGAGACCTGCTCTGAACTGGAGTCTGG 881

6 ProProGluProPArgTInaSpProProGlnProProArgProAspAspProTyrPro 80
 882 CCCCCTGAACCGCCTTGAACGGATCTCTCTCAACTCTCCCGGCTGACGACCCTTGCGG 941

Dy 81 ALAgiyPtiGInPrProGiuaSnPrOTrPrProAlaProGiIuValAspaSnaArgPro 100
| | | | |
Db 942 GCAGACCCCGAGCCCCCAAGAAACCCTTGGCCTCCTTGCCTCGAGGTGGACAACCGACTT 100

Dy
LVLGSLGLNLPKPAASPLEUASPPTOPFARGTGGTLTYRAG 114

Dd
| | | | | | | | | | | | | | | | | |
1002 CAGCAGACCGACACTAGACCACCCGCCGGAGAAGTACAGA 1043

AX477396	2997 bp	DNA	linear	PAT 12-AUG-200
LOCUS				
DEFINITION	Sequence 10 from Patent WO0244375.			

VERSION	AX477396.1	GI:22216625
KEYWORDS		
SOURCE	Homo sapiens (human)	

REFERENCE

1. Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

TITLE Compositions and methods for diagnosing or treating psoriasis
JOURNAL Patent: WO 0244375-A 10 06-JUN-2002;
Celltech R & D, Inc. (US)

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/organism="Homo sapiens"
/mol_type="unassigned DNA"
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ORIGIN	
Alignment Scores:	

Score:	692.00	Matches:	114
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0

DB:	6	Gaps:	0
US-09-994-365-3 (1-114) X AX477396 (1-2997)			

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 |||||
 Db 2213 A G C G A G G C C A C C C T C T A C C C A C C C G A G A G A C C G A G A G C A G G T C C C A C A 227

QY 21 LEUPROGLINGLYPProProValProGLyaspProTrpProGLyAlaProProLeupheGlu 40
 |||||
 Db 2273 TTGGCTCAGGGCCCCCAGTCCCCGGTGAACCTTGCGCAGGGGGACCCCCCTCTTTGAA 233

Qy	41	Asp	Pro	Pro	Thr	Arg	Pro	Set	Arg	Pro	Trp	Arg	Asp	Leu	Pro	Glu	Trp	Val	Trp	60	
Db	2333	GAT	CTC	CGC	CTA	CCC	CGC	CGC	CTA	CGT	CCC	TGG	GAG	GAG	ACT	GCT	GAA	CTG	GAG	CTGG	2339

Dy 6 ProProGluPProProA^rGPhrasPProPGlinPProCArGPProAspSPProCtyPPro 80
Db 2393 CCCCTGAACCGCTAGAAcGGATCTCTCAACTCCCCGGCCTTGACGACCCTTGGCCG 245

QY	81	ALGLGIPROGLINPROGLINASPRTCTPPROGLALAPROGLIVALASPASNAIRP	100
Db	2453	GCAGGACCCAGCCGCCAAGAAACCCCTGCTGCTGCTGAGGTGGACACACCGACT	2512

DB	Sequence	Position
07	101 GAGGAGGACCAAGCTTGAAGCCACCCCGGAGAGATGACAGA	114
2513	101 GAGGAGGACCAAGCTTGAAGCCACCCCGGAGAGATGACAGA	2554

RESULT	7	-	
AX477390			
LOCUS			
DEFINITION			
AX477390	3001 bp	DNA	
Sequence 4 from Patent W0024475.		linear	PAT 12-AUG-2002

ACCESSION	AX477390.1
VERSION	GI:22216619
KEYWORDS	
SOURCE	Homo sapiens (human)

ORGANISM Homio sapiens; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1

Authors
Charmelley, P., Moss, P. and McEneaney, M.
Title
Compositions and methods for diagnosing or treating psoriasis
Patent: WO 0244375-A 4 06-JUN-2002;
Celltech R & D, Inc. (US)

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location/Qualifiers
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/organism="Homo sapiens"
/mol_type="unassigned DNA"

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Alignment Scores:	

Score:	692.00	Matches:	114
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0

DB:	6	Gaps:	0
US-09-994-365-3 (1-114) x AX477390 (1-3001)			

Qy 1 **1** **2** **3** **4** **5** **6** **7** **8** **9** **10** **11** **12** **13** **14** **15** **16** **17** **18** **19** **20**
 Db 2217 AGCGAGGACCACTCTCTCACCCACCGACGAGCGAGGAGGAGGCGCTCCCAACA 2276

QY	21	40
Db	LeuProGlnGlyProPheValProGlyAspProTyrProGlyValAlaProProLeuPheGlu	
	TTGCTCAGGGGCCCCAGTCCCCGGTGAACCTTGGCAGGGGACACCCCTCTCTTGAA	2336

	Gy	41	ASPProProThrArgProSerArgProIrrpaGAspleuProGluThnClYValTyr	60
	Db	2337	GANCTCCGGCCTAACCGGCCAGTCGTCCCTGGAGAGACCTGCCTGAACAATGAAAGTTGG	2396

Qy	61	ProProGluProProArgThiAspProProGlnProProArgGProAspAspProTTPPro	80
Db	2397	CCCCCTGACCGCCTTGAACGGATCTCTCTCAACCTCCCGGCTTACGACCCCTTGCCCG	2456

Qy	Db
81	100
2457	2516

Qy	G	I	N	G	L	U	P	C	A	S	P	L	E	A	N	P	R	O	P	R	A	T	G	L	U	G	L	U	T	y	r	a	r	g		114
Db																																		2517		
	C	A	G	G	A	G	C	C	A	G	C	C	T	T	A	G	A	C	C	C	C	C	C	G	G	G	A	A	G	T	A	C	A	A	2558	

LOCUS	BD095297	25235 bp	DNA	linear	PAT 27-AUG-2002
DEFINITION	The method of testing for psoriasis vulgaris.				
ACCESSION	BD095297				
VERSION	BD095297.1	GI:22640885			
KEYWORDS	MO 0142458-A/2.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
AUTHORS	1 (bases 1 to 25235)				
TITLE	Inoko,H. and Tamiya,G.				
JOURNAL	The method of testing for psoriasis vulgaris				
COMMENT	Patent: WO 0142458-A 2 14-JUN-2001; HIDETOSHI INOKO, GEN TAMIYA OS HOMO SAPIENS (human) PD WO 0142458-A/2 PN 14-JUN-2001 PP 06-DEC-2000 WO 2000JP008624 PR 06-DEC-1999 JP 99P 346867 PI HIDETOSHI INOKO, GEN TAMIYA PC C12N15/12, C12Q1/68 CC The method of testing for psoriasis vulgaris FH Key FT exon Location/Qualifiers FT exon (11).. (420) FT exon (1282).. (1405) FT exon (1602).. (1702) FT exon (1602).. (1631) FT exon (2352).. (2364) FT exon (6287).. (6509) FT exon (10417).. (10493) FT exon (14244).. (14407) FT exon (14244).. (14344) FT exon (25190).. (25235).				
FEATURES	Location/Qualifiers 1..25235 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606"				
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Alignment Scores:					
Pred. No.:	6,14e-19	Length:	25235		
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Percent Similarity:	100.00%	Conservative:	0		
Best local Similarity:	100.00%	Mismatches:	0		
Query Match:	100.00%	Indels:	0		
DB:	6	Gaps:	0		
US-09-994-365-3 (1-114) x BD095297 (1-25235)					
QY	1	SergluglYHtAProSerHtAProProAlaglAgluAaPAGglugluAlaglYseProthr	20		
Db	1766	AGCGAGGCGCACCCCTCTACCCACCCGCAAGAGACGAGAGGCGAGGCTCCCAACA	18235		
QY	21	LeuProgingluYProProValProglYAsPProTrpProglYAlaProProLeuPhgglu	40		
Db	1826	TTGGCTCAGGAGCCCGCCGAGTCGCCCGGTACCCCTTGCCAGGAGGACCCCTCTTTGAA	18855		
QY	41	AsPProPProPProthtAaPProSerAaPProTrpAaPLeuAaPLeuProgluThGlyValTrp	60		
Db	1886	GATCTCCGCTACCCGCGCCCAAGTCGTCCCTCGAGAGACCTGCGTGAACCTGGAGTCTGG	19455		
QY	61	ProProgluPProPProAaPThAaPProProgluPProPProAaPProAaPProTrpPro	80		
Db	1946	CCCCCTGAACCGCCCTAAGACGATCTCTCAACTCCCGCGCTGACGACCCCTTGGCGG	20055		
QY	81	AlaglYProgluPProProgluAaPProTrpProProAlaPProgluValAaPAsAaPPro	100		
Db	2006	GCAAGACCCCAAGCCCGCCGAGAAAACCCCTGGCTCTGCGCCCTGAGGTGACACGACCT	20655		
QY	101	GlnglugluPProAaPLeuAaPProProAaPProAaPProgluYTrpAaP	114		

Db 2066 CAGAGGAGCCAGACCTAGACCCACCCCGGAGAGTACAGA 2107

RESULT 9	AB088114/c	30911 bp	DNA	linear	PRI 08-JAN-2003
LOCUS	AB088114/c				
DEFINITION	Homo sapiens STG, S, SPR1, SEEK1 genes.				
ACCESSION	AB088114				
VERSION	AB088114.1	GI:27544424			
KEYWORDS					
ORGANISM	Homo sapiens (human)				
SOURCE	Homo sapiens				
REFERENCE	Eukaryotic: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
AUTHORS	Shima,T., Ota,M., Katsuyama,Y., Haashimoto,N. and Inoko,H.				
TITLE	Genome diversity in HLA: A new strategy for detection of genetic polymorphisms in expressed genes within the HLA class III and class I regions				
JOURNAL	Unpublished				
REFERENCE	2 (bases 1 to 30911)				
AUTHORS	Shima,T.				
TITLE	Direct Submission				
JOURNAL	Submitted (08-JUL-2002) Takaashi Shima, Tokai University School of Medicine, Molecular Life Science 2; Bohseida, Iehara, Kanagawa 253-1193, Japan (E-mail:tachina@is.icc.u-tokai.ac.jp, Tel:81-463-93-1121, Fax:81-463-94-8884)				
FEATURES	Location/Qualifiers				
SOURCE	1. 30911				
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	/number=2				
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exon	10423. .10521	PSNNIIPQSAAASAIARFQVGTGAVQLCGGGTSGKSPSPSSSRVPSSSSISSSS
exon	/number=1	GSPPHRCGASQSPCSPTROTGGTFSSSSSSSGKTIILPPCSKSSSSHPICMVSLSLT
exon	15765. .15928	LITGGDPSGHPDPDSAGAKPCGSSSAGKIPCSIRKILAQVXPLQLADPEVFLPQES
exon	19676. .19752	LIDSPr
exon	/number=2	27641. .28413
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ORIGIN		
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Percent Similarity:	100.00%	Conservative: 0
Best local Similarity:	100.00%	Mismatches: 0
Query Match:	100.00%	Indels: 0
DB:	9	Gaps: 0
US-09-994-365-3 (1-114) x AB088114 (1-30911)		
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QY	21	LeuProGInglYProProValProGlyAspProTrpProGlyValaProPoleuPheGlu 40
Db	28342	TTGCTCTAGGGCCCCCAAGTCCCGGAGACCTTGGCCAGAGGACACCCCTCTTTGAA 28283
QY	41	AspProProThrIaArgProSerArArgProTrpArgAspLeuProGluThrGlyValTrp 60
Db	28282	GATCCTCGGCTACCGCCCAAGTCGTCCTCGAGAGACCTGCTGAAACTGAGAGCTGG 28222
QY	61	ProProGluInProPAlaGlyThrAspProProGlnProProArgProAlaAspProTrpPro 80
Db	28222	CCCCCTTAACCGCTAGAACGAGATCCTCTCAACCTCCCGGCTGACGACCTTGCCG 28163
QY	81	AlaGlyProGlnProProGluAsnProTrpProProAlaProGluValaAspAsnArgPro 100

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Db      28162  GCAGGACCCCGACGCCCCAGAAAAACCCCTGCGCTTCCTGCCCCCTTGAGTGGAACACGACCT 2810
Qy      101  GInGIuGIuPrOAsPLeuAsPPrOArGInGIuInTyArG 114
Db      28102  CAGGAGGAGCCAGACTTAGACCCACCCCGGAGAGATACAGA 28061
RESULT 10
DEFINITION Homo sapiens genomic DNA, chromosome 6p21.3, HLA class I region,
            clone:TY1C2, complete sequence.
ACCESSION AB023060
VERSION   AB023060.1 GI:5672629
SOURCE    HTG.
ORGANISM  Homo sapiens (human)
            Homo sapiens
            Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases)
AUTHORS   Shihna,T., Tamiya,G., Oka,A., Takishina,N., Yamagata,T.,
            Kikkawa,E., Iwata,K., Tomizawa,M., Okuaki,N., Kuwano,Y.,
            Watanabe,K., Fukuzumi,Y., Itakura,S., Sugawara,C., Ono,A.,
            Yamazaki,M., Tashiro,H., Ando,A., Ikemura,T., Soeda,E., Kimura,M.,
            Bahram,S. and Inoko,H.
            Molecular dynamics of MHC genesis unraveled by sequence analysis of
            the 1,796,938-bp HLA class I region
            Proc. Natl. Acad. Sci. U.S.A. 96 (23), 13282-13287 (1999)
JOURNAL   20027539
MEDLINE   10557312
REFERENCE 2 (bases 1 to 39196)
AUTHORS   Shihna,T. and Takishina,N.
TITLE      Direct Submision
            Submitted (29-JAN-1999) Takashi Shihna, Tokai University School of
            Medicine, Department of Molecular Life science 2, Bohseidai,
            Isehara, Kanagawa 259-1193, Japan
            (E-mail:shihna@is.tcc.u-tokai.ac.jp, Tel:81-463-93-1121,
            Fax:81-463-94-8884)
FEATURES
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ORIGIN
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Score:          692.00      Matches:      114
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:    100.00%      Indels:      0
DB:             Gaps:      0
US-09-994-365-3 (1-114) x AB023060 (1-39196)
Qy      1  SerGIuGIuHAsPProSerHAsPProALaGIuAsPArGIuGIuALaGIySerProThr 20
Db      10646  AGCGAGGGGCCACCCCTCAACCCAGCGAGACCGAGAGAGAGAGAGCGGTCCCCAACCA 10705
Qy      21  LeuProGIuGIuPrOProValProGIuAsPProTPrProGIuAlAProProLeuPheGIu 40
Db      10706  TTGCCTCAAGGGCCCCCAAGTCCCGGTGACCTTGCGCAGGGGCAACCCCTCTTTTAA 10765
Qy      41  AspProProProThrArGrProSerArGrProTLpArGAsPLeuProGIuThnGIyValTrp 60
Db      10766  GATCCTCGCGCTACCGGCCCGCGTGTCTCCCTGGAAGACCTGCTCGAATCGAATCTGG 10825
Qy      61  ProProGIuPrOProArGrThAsPProProGIuPrOProArGrProAsPPrOTrPrPro 80

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Df	10826	CCCCCTGACCGCCTAGAACGGANCCCTTCACACCTCCGCCGCCTACACGACCCTTGCGCG	108855
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Df	10886	GACAGACCCCACGCCCCCAAAAAACCCCTGCGCTTCCTGCCCCCTGAGGTGGAACAACGACCT	10945
Oy	101	GInGluGlnPheAspLeuAspProPheArgGluGluTyrArg	114
Df	10946	CAGAGAGACCGACCTTAGACCCACCCCGGAAAGATGACGA	10987
<div style="text-align: center;">RESULT 11 AC004195</div>			
LOCUS	AC004195	40878 bp	DNA linear PRI 08-DEC-1998
DEFINITION	Homo sapiens clone UMGc:y24c027 from 6p21, complete sequence.		
ACCESSION	AC004195		
VERSION	AC004195.1	GI:3980474	
KEYWORDS	HTG.		
SOURCE	Homo sapiens		
ORGANISM	Homo sapiens (human)		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
TITLE	1 (bases 1 to 40878)		
JOURNAL	Jerar,M., Gulllaudeux,T., Vu,Q., Kutayvin,T., Harter,H. and Geraghty,D.E.		
REMARK	Large scale sequence analysis of the human MHC class I region Unpublished (1998) Fred Hutchinson Cancer Research Center The Clinical Research Division 1100 Fairview Ave. N., P.O. Box 19024 Seattle, WA 98109-1024 Contact: Daniel E. Geraghty (geraghty@fhcrc.org)		
REFERENCE	2 (bases 1 to 40878)		
AUTHORS	Geraghty,D.E. and Olson,M.V.		
TITLE	Direct Submission		
JOURNAL	Submitted (23-FEB-1998) Human Genome Center, University of Washington, Box 352145, Seattle, WA 98195, USA		
REFERENCE	3 (bases 1 to 40878)		
AUTHORS	Geraghty,D.E. and Olson,M.V.		
TITLE	Direct Submission		
JOURNAL	Submitted (08-DEC-1998) Human Genome Center, University of Washington, Box 352145, Seattle, WA 98195, USA		
REMARK	University of Washington Human Genome Center Box 352145 Seattle, WA 98195 Contact: Daniel E. Geraghty (geraghty@fhcrc.org) On Dec 8, 1998 this sequence version replaced gi:2905865. Overlapping Sequences:		
COMMENT	5': UMGc:y14c057 (Genbank Accession: AC006047) 3': UMGc:y24c203		

Sequence Quality Assessment:			
This entry has been annotated with sequence quality estimates computed by the Pirap assembly program. All manually edited bases have been reduced to quality zero. Quality levels above 40 are expected to have less than 1 error in 10,000 bp.			
Base-by-base quality values are not generally visible from the Genbank flat file format but are available as part of this entry's ASN.1 file.			

Double stranded (DS) coverage: 77.6%			
DS or two chemistry coverage: 100.0%			
Single stranded regions: 0			

Sequence Validation:			
This sequence has been validated by Multiple Complete Digest Mapping. Comparison of the experimentally derived map digest fragments with sequence-predicted fragments is given below. Small fragments below a variable cutoff (approximately 400-600bp) are not mapped and hence do not appear in the table. There are no significant remaining discrepancies between the experimental and predicted values. Uniquely ordered fragment groups are separated by dashed lines.			
BgIII HindIII NotI			

	Map	Seq	Map	Seq	Map	Seq
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	894.03	880.00	4618.79	4525.00	10116.87	9863.00
	3041.57	2999.00	1532.79	1530.00	2432.75	2413.00
	14697.70	14691.00	1726.25	1724.00		
			1479.40	1473.00		
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corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em, EMBL; Sw, SWISSPROT; Tr, TrEMBL; Wp, WormPEP; information on the WormPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep XXbac-34D1 is from a CHORI-502 human bac - COX cell line library VECTOR: PTARAC2.1

This sequence was generated from part of bacterial clone contigs constructed by the MHC HaploType Consortium and collaborators. Further information can be found at <http://www.sanger.ac.uk/HGP/Chr6/MHC>.

FEATURES

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ORIGIN

Alignment Scores:

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Query Match:	100.00%	Indels:	0
DB:	9	Gaps:	0

US-09-994-365-3 (1-114) x AL662867 (1-70288)

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 QY 21 LseProGlnGlyProProValProGlyA8PArgProTrrProGlyAlaProProLeuA8PheGlu 40
 Db 67651 TTGGCTCAGGAGCCGCCAGTCCCGGTGACCTTGGCCAGGGGACCCCTCTCTTGAA 67592
 QY 41 AspProProBroThrArgProSerArgProTrrArgA8PleuA8PProGlnArgLValTrrp 60
 Db 67591 GATCCTCCGCTACCCGCCAGTCCCTCGAGAGACCTGGCTGAACTGGAGTCTGG 67532
 QY 61 ProProGluProProArgThrArgProProGlnProProArgProA8PArgProTrrPro 80
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 QY 81 AlaGlyProGlnProProGluA8PProTrrProProAlaProGluValA8PArgPro 100
 Db 67471 GCGAGACCCAGCCGCCAAGAAACCTTGGCTCTCTGCCCCCTGAGTGGACACCGACT 67412
 QY 101 GlnGluGluProA8PleuA8PProProArgGluGluTrrArg 114
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RESULT 14
 AP000510
 LOCUS AP000510 99999 bp DNA linear PRI 22-AUG-2001
 DEFINITION Homo sapiens genomic DNA, chromosome 6p21.3, HLA Class I region,
 section 9/20.
 ACCESSION AP000510 BA000025
 VERSION AP000510.2 GI:7380878
 KEYWORDS
 SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1 Shima, S., Tamiya, G., Oka, A. and Inoko, H.
 Homo sapiens 2,229,817bp genomic DNA of 6p21.3 HLA class I region
 Published only in Database (1999)
 2 (bases 1 to 99999)
 Hirakawa, M., Yamaguchi, H., Imai, K. and Shimada, J.
 Direct Submission
 Submitted (21-SEP-1999) Mika Hirakawa, Japan Science and Technology
 Corporation (JST), Advanced Databases Department; 5-3, Yonbancho,
 Chiyoda-ku, Tokyo 102-0081, Japan (E-mail: mika@okyo.jst.go.jp,
 URL: <http://www-alis.tokyo.jst.go.jp/>, Tel: 81-3-5214-8491,
 Fax: 81-3-5214-8470)

COMMENT

On Mar 31, 2000 this sequence version replaced gi:5926697.
 This sequence is conducted by Tokai University as a JST sequencing
 Team.
 Principal Investigator: Hidetoshi Inoko Ph.D
 Phone: +81-463-93-1121, Fax: +81-463-94-8884,
 The sequence is submitted by Human Genome Sequencing in ALIS
 project of JST
 Japan Science and Technology Corporation (JST)
 5-3, Yonbancho, Chiyoda-ku, Tokyo, 102-0081 Japan
 For further information about this sequences, please visit our
 sequence archive Web site (<http://www-alis.tokyo.jst.go.jp/HGS/top.html>) or send email to webmaster@www-alis.tokyo.jst.go.jp
 Sequence updated (28-Mar-2000).

FEATURES

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US-09-994-365-3 (1-114) x AL773544 (1-113388)

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QY      21 LeuProGluGlyProProValProGlyAspProTyrProGlyAlaProProLeuPheGlu 40
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QY      41 AspProProProThrArgProSerArgProTyrArgAspLeuProGluThrGlyValTyr 60
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Db      60011 GATCCTCCGGCTACCCGCGCAGTGTCTCGAGAGAGACCTGCTGAACCTGGAGTCTGG 59952
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QY      61 ProProGluProProArgThrAspProProGluProProArgProAspAspProTyrPro 80
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QY      81 AlaGlyProGluProProGluAsnProTyrProProAlaProGluValAspAsnArgPro 100
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Db      59891 GCAGGACCCGAGCCCGCAAAACCCCTGGGCTCTGCCCCCTGAGGTGACCAACGACCT 59832
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QY      101 GluGluGluProAspLeuAspProProArgGluGluTyrArg 114
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GenCore version 5.1.6
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OM protein - nucleic search, using frame_p2n model

Run on: January 11, 2005, 10:41:32 ; Search time 3693.76 Seconds
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Fgapop 6.0, Fgapext 7.0
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Minimum DB seq length: 0
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	808	100.0	1143	CQ722444	Sequence
3	808	100.0	1143	AB031480	Homo sapi
4	808	100.0	1185	AF484420	Homo sapi

5	808	100.0	1473	AX406002	Sequence
6	712	88.1	2997	AX477396	Sequence
7	712	88.1	3001	AX477390	Sequence
8	712	88.1	25235	BD095297	the metho
9	712	88.1	30911	AB088114	
10	712	88.1	39156	AB023060	Homo sapi
11	712	88.1	50878	AC004195	Homo sapi
12	712	88.1	55050	AX522117	Sequence
13	712	88.1	70288	AL662867	Human DNA
14	712	88.1	99999	AP000510	Homo sapi
15	712	88.1	113388	AL773544	Human DNA
16	712	88.1	135396	BX927139	Human DNA
17	712	86.9	204238	AL662844	Macaca mu
18	686	84.9	175689	AC148703	Macaca mu
19	682	84.4	300050	AB100083	Pan trogl
20	672	83.2	200068	AC148691	Macaca mu
21	617	76.4	383	AF484422	Sus bctof
22	588	72.8	154749	AB113354	Sus bctof
23	573.5	71.0	809	AF484421	Mus muscu
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25	522	64.6	349571	AX978973	Mus muscu
26	516.5	63.9	1377	AF159090	Rattus no
27	516.5	63.9	159179	AF159090	Mus muscu
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29	449	55.6	349980	AX344554	Sequence
30	304.5	37.7	248	AR418279	Sequence
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36	208	25.7	185549	BX927317	Danio rer
37	207.5	25.7	152340	CR396595	Danio rer
38	206.5	25.6	91040	BX248094	Zebrafish
39	206.5	25.6	166514	BX469924	Zebrafish
40	205	25.4	177205	CR376782	Danio rer
41	205	25.4	185411	BX548008	Danio rer
42	205	25.4	225024	CR394539	Danio rer
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44	204	25.2	242992	BX567988	Danio rer
45	203.5	25.2	161366	BX005382	Zebrafish

ALIGNMENTS

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DEFINITION	Sequence 1 from Patent WO0244375.				
ACCESSION	AX477387				
VERSION	AX477387.1	GI:22216617			
KEYWORDS					
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ORGANISM	Homo sapiens (human)				
REFERENCE	Charnley, P., Moss, P. and Mcewen, M.				
AUTHORS	Charnley, P., Moss, P. and Mcewen, M.				
TITLE	Compositions and methods for diagnosing or treating psoriasis				
JOURNAL	Patent: WO 0244375-A 1 06-JUN-2002;				
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ORIGIN

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Alignment Scores:

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 Score: 808.00 Matches: 136
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 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0

US-09-994-365-2 (1-136) x AX477387 (1-891)

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 Db TCAGGACGAGAGGAGCCACCTCTCAACCCGACAGAGACGAGAGGAGGAGGCTCC 183
 Qy 41 ProThreupProGlnGlyProProValProGlyAspProTTPProGlyAlaProProleu 60
 Db CCAACATTGCTCAAGGAGCCGCCAGTCCCGTGAACCTTGCCAGGAGGAGCCCTCTC 243
 Qy 61 PheGluAspProProProThraArgProSerArgProTTPArgAspLeupProGlyuThrgly 80
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 Qy 81 ValTTPProGlyuProProArgThraPaspProProGlnProProAlaPaspAspPro 100
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 Qy 101 TTPProAlaGlyProGlnProProGluAsnProTTPProProAlaPaspAspPro 120
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RESULT 2
 LOCUS CQ722444 1143 bp DNA linear PAT 03-FEB-2004
 DEFINITION Sequence 8378 from Patent WO02068579.
 ACCESSION CQ722444
 VERSION CQ722444.1 GI:42283301
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1
 Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.
 Kites, such as nucleic acid arrays, comprising a majority of
 humanexons or transcripts, for detecting expression and other uses
 thereof
 Patent: WO 02068579-A 8378 06-SEP-2002;
 JOURNAL PE Corporation (NY) (US)
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ORIGIN

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US-09-994-365-2 (1-136) x CQ722444 (1-1143)

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 Db TCAGGACGAGAGGAGCCACCTCTCAACCCGACAGAGACGAGAGGAGGAGGCTCC 435
 Qy 41 ProThreupProGlnGlyProProValProGlyAspProTTPProGlyAlaProProleu 60
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 Db TTTGAGATCCTCGGCTCAACCGCCAGTCCGCTCGAGAGACCTGCTGAACCTGGA 555
 Qy 81 ValTTPProGlyuProProArgThraPaspProProGlnProProAlaPaspAspPro 100
 Db GTCTGGCCCTCAACCGCTCAACCGATCTCTCAACCTCCCGCTGACGACCTC 615
 Qy 101 TTPProAlaGlyProGlnProProGluAsnProTTPProProAlaPaspAspPro 120
 Db TGGCCGAGAGAGAGCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 675
 Qy 121 ArgProGlnGlyuProAspLeuAspProProArgGlyuGlyuYzarg 136
 Db CGACCTCAG 723

RESULT 3
 LOCUS AB031480 1143 bp mRNA linear PRI 08-DEC-1999
 DEFINITION Homo sapiens SPRI mRNA, complete cds.
 ACCESSION AB031480
 VERSION AB031480.1 GI:6539433
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (sites)
 Oka, A., Tamliya, G., Tomizawa, M., Oka, M., Katsuyama, Y., Makino, S.,
 Shina, T., Yoshitome, M., Iizuka, M., Saseo, Y., Iwashita, K.,
 Kawakubo, Y., Sugai, J., Ozawa, A., Ohkido, M., Kimura, M., Bahram, S.
 and Inoko, H.
 Association analysis using refined microsatellite markers localizes
 a susceptibility locus for psoriasis vulgaris within a 111 kb
 segment telomeric to the HLA-C gene
 Hum. Mol. Genet. 8 (12), 2165-2170 (1999)

JOURNAL MEDLINE
 PUBMED 1054595
 TITLE 2 (bases 1 to 1143)
 AUTHORS Tamliya, G., Tomizawa, M., Makino, S., Oka, A., Nakajima, K., Kimura, M.
 and Inoko, H.
 Direct Submision
 Submitted (25-AUG-1999) Akira Oka, Tokai University School of
 Medicine, Division of Molecular Life Science, Bohseidai, Isehara,
 Kanagawa 259-1193, Japan (E-mail: oka246@s.icc.u-tokai.ac.jp,
 Tel: 81-463-93-1121 (ex.2579), Fax: 81-463-94-8884)

FEATURES
 source 1. .1143
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
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 /gene="SPRI"
 316. .726

gene
 CDS
 316. .726

/gene="SPR1"
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/protein_id="BA08131.1"
/db_xref="GI:6539434"
/translation="MILNWKILGILVLCIHTRGISGSEGHPSHPADREAGSPPLP
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325..735
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AGQPENPWPAPAEVDNRPQEBPDLDPPREYR"

ORIGIN

Alignment Scores:

Prod. No.:	2.49e-24	Length:	1143
Score:	808.00	Matches:	136
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	9	Gaps:	0

ORIGIN

US-09-994-365-2 (1-136) x AB031480 (1-1143)

QY 1 MetIleuAantTpyLsleuLeuGlylleuValleuCyseuHisThrArgGlylle 20
Db 316 ATGATCTCAACTGGAAGCTCTGGGATCTGTGCTTGGCCGACACCAAGAGGATC 375
QY 21 SerGlySerGluGlyHisProSerHisProProAlaGluAspArgGluAlaGlySer 40
Db 376 TCAGGCGACGAGGGCCACCCCTCTCACCCGACAGAGACCGAGAGGAGCGCTCC 435

QY 1 MetIleuAantTpyLsleuLeuGlylleuValleuCyseuHisThrArgGlylle 20
Db 325 ATGATCTCAACTGGAAGCTCTGGGATCTGTGCTTGGCCGACACCAAGAGGATC 384
QY 21 SerGlySerGluGlyHisProSerHisProProAlaGluAspArgGluAlaGlySer 40
Db 385 TCAGGCGACGAGGGCCACCCCTCTCACCCGACAGAGACCGAGAGGAGCGCTCC 444
QY 41 ProThrIeuProGluGlyProProValProGlyAspProTrpProGlyAlaProProLeu 60
Db 445 CCAACATTTGGCTCAGAGGCCCCCGGATCCCGGATGACCTTGGCCAGAGGAGCCCCCTCTC 504
QY 61 PhgGluAspProProProThrArgProSerArgProTrpArgAspLeuProGluThrGly 80
Db 505 TTTGAAGATCTCTCGCTTACCGCCGATGCTCTCGAGAGAACCTGCTGAATCTGA 564
QY 81 ValTrpProProGluProProArgTrpAspProProGluProProArgProAspAspPro 100
Db 565 GTCTGGCCCCCTGAACCGCTTGAACGATCTCTCACTCTCCCGGCTGACGACCT 624
QY 101 TrpProAlaGlyProGluProProGluAspProTrpProProAlaProGluValAspAsn 120
Db 625 TGGCCGCGACAGACCCGACCCCAAGAAAACCCCTGGGCTCTGCCCCCTGAGGTGACAA 684
QY 121 ArgProGluGluGluProAspLeuAspProProArgGluGluGlyArg 136
Db 685 CGAAGCTCAGAGAGAGCCAGACTTGAACCCCGGAGAGAGTACAGA 732

RESULT 4
AF484420 1185 bp mRNA linear PRI 02-MAR-2003
LOCUS Homo sapiens psoriasis susceptibility 1 candidate 2 (PSORS1C2)
DEFINITION mRNA, complete cds.
ACCESSION AF484420
VERSION AF484420.1 GI:28628834
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1185)
AUTHORS Holm,S.J., O'Brien,K.P., Carlen,L. and Stahle-Backdahl,M.
TITLE The PSORS1C1 and PSORS1C2 genes in 6p21.3 associate strongly with
psoriasis in the Swedish population
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1185)
AUTHORS Holm,S.J., O'Brien,K.P., Carlen,L. and Stahle-Backdahl,M.
TITLE Direct Submission
JOURNAL Submitted (15-FEB-2002) Dermatology, Karolinska Institute, L8:02
Karolinska Sjukhuset, Stockholm S-17176, Sweden
FEATURES
SOURCE 1.1185
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"

RESULT 5
AX406002 1473 bp DNA linear PAT 14-JUN-2002
LOCUS Sequence 417 from Patent WO0222660.
DEFINITION AX406002
ACCESSION AX406002
VERSION AX406002.1 GI:21439443
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS Tang,Y.T., Liu,C., Zhou,P., Asundi,V., Zhang,J., Zhao,Q.A., Ren,F.,
Xue,A.J., Yang,X., Wehrman,T. and Drmanac,R.T.
TITLE Novel nucleic acids and polypeptides
JOURNAL Patent: WO 0222660-A 417 21-MAR-2002;
HYSEQ, INC. (US)
Location/Qualifiers

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/note="unnamed protein product"
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GQPVPGDPMGAPPLFEDPPPTPSRRWRLPPTGVWPPPPPTDPPQPPRPDPMW
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ORIGIN

Alignment Scores:
Pred. No.: 2.98e-24 Length: 1473
Score: 808.00 Matches: 136
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatch: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-994-365-2 (1-136) x AX406002 (1-1473)

QY 1 MetIleLeuAaNTpLyLeuLeuLylIleLeuValIleCySleuH:ThrArgGlyIle 20
Db 636 ATGATCTCAACTGGAAAGCTCTGGAGATCTCTGTCTTGTGCTTCAACACAGAGGCTC 695
QY 21 SerGlySerGluGluYHAsProSerHAsProFroAlaGluAspArgGluGluAlaGlySer 40
Db 696 TCAGGCAAGAGGGCCACCCCTCTCACCACCCGAGAGACCGAGAGAGGCAAGGCTCC 755
QY 41 ProThrLeuProGlnGlyProProValIProGlyAspProTTPProGlyAlaProProLeu 60
Db 756 CCAACATTGCTCAGAGGGCCCCCAATCTCCCGGTGACCTTTGGCCAGGGGCAACCCCTCTC 815
QY 61 PheGluAspProProProThrArGProSerArGProTPArGAspLeuProGluThrGly 80
Db 816 TTGAGATCTCTCCGCTTACCGCCCAAGTGTCTCTTGAAGACCTCTCGTAAACTGGA 875
QY 81 ValTTPProProGluProProArGThrAspProProGlnProProArGProAspAspPro 100
Db 876 GTCTGGCCCCCTGAACCGCTTGAAGCGATCTCTCAACCTCCCGGCGCTGACGACCTT 935
QY 101 TTPProAlaGlyProGlnProProGluAsnProTTPProProAlaIProGluValAspAsn 120
Db 936 TGGCCGCGAGAACCCCAAGCCCAAGAAAAACCCCTGCTCTGCCCCCGAGGTGACAAAC 995
QY 121 ArgProGlnGluGluProAspLeuAspProProArGArgGluGluTyrArg 136
Db 996 CGACCTCAGAGAGAGCCAGACCTTGAACCCACCCCGGAAAGATACAGA 1043

RESULT 6
AX477396 2997 bp DNA linear PAT 12-AUG-2002
DEFINITION Sequence 10 from Patent WO0244375.
VERSION AX477396
ACCESSION AX477396
KEYWORDS GI:22216625
SOURCE
.
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 Charmley, P., Mose, P. and Meuen, M.
AUTHORS Compositions and methods for diagnosing or treating psoriasis
TITLE Patent: WO 0244375-A 10 06-JUN-2002;
JOURNAL Celltech R & D, Inc. (US)
FEATURES
location/Qualifiers
1..2997
/organism="Homo sapiens"
/mol_type="unassigned DNA"
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Score: 712.00	Matches: 118				
Percent Similarity: 100.00%	Conservative: 0				
Best Local Similarity: 100.00%	Mismatches: 0				
Query Match: 88.12%	Indels: 0				
DB: 6	Gaps: 0				
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US-09-994-365-2 (1-136) x AX477396 (1-2997)					
Oy	19 GlyIleSerGlySerGIUGLIYhiAProSeXhiSProfoalagluAAsPaRGluGLUla	38			
Dd	2201 GGCACTCAGGCACGAAGGGCCACCCTCTCACCAccCGAGAgaGCCAgAGAGCCA	2260			
Oy	39 GlysErPrOThLeUPrOGInGlYPPrOPrOVAlProlglYAbspOTTPrOGlYaLaPRo	58			
Dd	2261 GGCTCCCACAATGTGCCTCAGgggCCCCcCATTCcccGGTGAcCCTTGgcCAggGGCAccc	2320			
Oy	59 ProteuhneGUAbPPROPrOPRothARgPROseRaRPROTtpAGApLEUpRoGLU	78			
Dd	2321 CCTCTTTGAAGAcTCtCcCGCCTAACCCGCCCAgtGTcCTctGaAGACTtcCTCaAA	2380			
Oy	79 ThrgLYALtTpRpOpROgLUPrOPrArghThzASBPprOfGINPrOPrOAgrPIOASP	98			
Dd	2381 ACTGGAGCTGTGccccCTGAAccCCCTTAAGAAGSATCTCCTCAACTccccGScTGAC	2440			
Oy	99 ASBPrOtTPrOAlaglYPPrOGlnPrOPrOGluAnDPrOTTPrOPrOAlapROgluaVl	118			
Dd	2441 GAacCTTGcgCGGAGAGACCCCAccCCCAAAAaccCTtgCcCTCGCCCTGAAGGTG	2500			
Oy	119 AsPBmARGPrOGlngLUgnLUPrOBsLeubASBPPrObArgSLunTYZARg	136			
Dd	2501 GACAAcCGACCTCAGAGAGAGCCAGACTTAGACCCACCCGGGAAGATAcAGA	2554			
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RESULT 7					
AX477390					
LOCUS	AX477390	3001 bp	DNA	linear	PAT 12-AUG-2002
DEFINITION	Sequence 4 from Patent WO0244375.				
ACCESSION	AX477390				
VERSION	AX477390.1 GI:22216619				
KEYWORDS	.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo. Charmley P., Moss P. and Mceuen M. Compositions and methods for diagnosing or treating psoriasis Patent: WO 0244375-A 4 Oct-2002; Celltech R & D, Inc. (US) Location/Qualifiers				
FEATURES	source	1..3001			
ORIGIN	/organism="Homo sapiens" /mol_type="unasigned DNA" /db_xref="taxon:9606"				
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Score: 712.00	Matches: 118				
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Best local Similarity: 100.00%	Mismatches: 0				
Query Match: 88.12%	Indels: 0				
DB: 6	Gaps: 0				
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US-09-994-365-2 (1-136) x AX477390 (1-3001)					
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Dd	2205 GGCACTCAGGCACGAAGGGCCACCCTCTCACCAccCGAGAgaGCCAgAGAGCCA	2264			

Qy 39 G1ySerProThreupProginglyProProValProG1yAAspProTTPProG1yAlaPro 58
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|
|
Db 2265 GGCTCCCCAATTGGCTCAGGGGCCCCAGTCCCGGTGACCTTGCCAGGGGACACC 2324
|
|
|
Qy 59 ProleuphegluAAspProProProThraYgProSerArGProTTPAgaApleuProglu 78
|
|
|
Db 2325 CCTCTCTTTAAAGATCTCCGCCCTACCGCCAGTGTCTCCAGAGACCTGCCGAA 2384
|
|
|
Qy 79 ThG1yAlaTTPProProG1uPProProArGThraAAspProProG1nPProProArGProAAsp 98
|
|
|
Db 2385 ACTGAGATCTGGCCCCCTGAACCCCTAGAACGATCTCTCAACTCCCGGCGCTGAC 2444
|
|
|
Qy 99 AspProTTPProAlaG1yProG1nPProProG1uAAspProTTPProProAlaProG1uVal 118
|
|
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Db 2445 GACCCCTTGGCGGAGAGACCCCAAGAAACCCTGGCTCTCGCCCTGAGGTG 2504
|
|
|
Qy 119 AspAAspArGProG1uG1uPProAAspApleuAAspProProArG1uG1uYrArG 136
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|
|
Db 2505 GACAAACGACCTCAGAGAGACCAAGACTAGACCACCGGGAAGATACAGA 2558
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|
|
RESULT 8
LOCUS BD095297 25235 bp DNA linear PAT 27-AUG-2002
DEFINITION The method of testing for psoriasis vulgaris.
ACCESSION BD095297
VERSION BD095297.1 GI:22640865
KEYWORDS WO 0142458-A/2.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 25235)
AUTHORS Inoko, H. and Taniya, G.
TITL The method of testing for psoriasis vulgaris
JOURNAL Patent: WO 0142458-A 2 14-JUN-2001;
HIDETOSHI INOKO, GEN TANIYA
COMMENT OS Homo sapiens (human)
PN WO 0142458-A/2
PD 14-JUN-2001
PF 06-DEC-2000 WO 2000JP008624
PR 06-DEC-1999 JP 99P 346867
PI HIDETOSHI INOKO, GEN TANIYA
PC C12N15/12, C1201/68
CC The method of testing for psoriasis vulgaris
FH Key Location/Qualifiers
FT exon (1) .. (420)
FT exon (1282) .. (1405)
FT exon (1602) .. (1702)
FT exon (1602) .. (1631)
FT exon (2352) .. (2364)
FT exon (6287) .. (6509)
FT exon (10417) .. (10493)
FT exon (14244) .. (14407)
FT exon (14244) .. (14344)
FT exon (25190) .. (25235).
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source location/Qualifiers
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Pred. No.: 1.4e-19 Length: 25235
Score: 712.00 Matches: 118
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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 88.12% Indels: 0
Gaps: 0
US-09-994-365-2 (1-136) x BD095297 (1-25235)
Qy 19 G1y1leSerGlySerG1uG1yH1sProSerH1sProProAlaG1uAAspArG1uG1uAla 38

Db 1754 GGCATCTCAGGCGAGGCGCCACCCCTTACACCACCCGACAGAGAGAGAGAGCA 1813
|
|
|
Qy 39 G1ySerProThreupProginglyProProValProG1yAAspProTTPProG1yAlaPro 58
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|
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Db 1814 GGCTCCCCAATTGGCTCAGGGGCCCCAGTCCCGGTGACCTTGCCAGGGGACACC 1873
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|
|
Qy 59 ProleuphegluAAspProProProThraYgProSerArGProTTPAgaApleuProglu 78
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Db 1874 CCTCTCTTTAAAGATCTCCGCCCTACCGCCAGTGTCTCCAGAGACCTTGCGAA 1933
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|
Qy 79 ThG1yAlaTTPProProG1uPProProArGThraAAspProProG1nPProProArGProAAsp 98
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Db 1934 ACTGAGATCTGGCCCCCTGAACCCCTAGAACGATCTCTCAACTCCCGGCGCTGAC 1993
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Qy 99 AspProTTPProAlaG1yProG1nPProProG1uAAspProTTPProProAlaProG1uVal 118
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Db 1994 GACCCCTTGGCGGAGAGACCCCAAGAAACCCTGGCTCTCGCCCTGAGGTG 2053
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|
Qy 119 AspAAspArGProG1uG1uPProAAspApleuAAspProProArG1uG1uYrArG 136
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|
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Db 2054 GACAAACGACCTCAGAGAGACCAAGACTAGACCACCGGGAAGATACAGA 2107
|
|
|
RESULT 9
LOCUS AB088114/c 30911 bp DNA linear PRI 08-JAN-2003
DEFINITION Homo sapiens STG, S, SPR1, SEEK1 genes.
ACCESSION AB088114
VERSION AB088114.1 GI:27544424
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS Shiina, T., Ota, M., Katsuyama, Y., Hashimoto, N. and Inoko, H.
TITL Genome diversity in HLA: A new strategy for detection of genetic
polymorphisms in expressed genes within the HLA class III and class
I regions
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 30911)
AUTHORS Shiina, T.
TITL Direct Submissions
JOURNAL Submitted (08-JUL-2002) Takaishi Shiina, Tokai University School of
Medicine, Molecular Life Science 2; Bohseida, Isehara, Kanagawa
259-1193, Japan (E-mail: tshiina@is.icc.u-tokai.ac.jp,
Tel:81-463-93-1121, Fax:81-463-94-8884)
FEATURES
source location/Qualifiers
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US-09-994-365-2 (1-136) x AB088114 (1-30911)

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Qy 39 G1ySeerProThrIeuProGIingIyProProAlaProGIyAspProTrpProGIyAlaPro 58

Db 28354 GGCTCCCAACATTGCTCTCAGGGCCCCCAGTGTCCCGGTGACCTTGCGCAGGGGGACCC 28295

Qy 59 ProIeuPheGIuAspProProProThaArgProSeerArgProTrpArgAspIeuProGIu 78

Db 28394 CCTCTCTTTAAATCCTCCGCTACCCGCCCAAGTCGTCCTCGAGAGACACTGCTGA 28235

Qy 79 ThrGIyAlaTrpProProGIuProProAlaArgThsAspProProGIuInProProAlaArgProAsp 98

Db 28234 ACTGAGATCTGGCCCCCTGAACCGCTTGAACGGAATCTCTTCACTCCCGGCTGAC 28175

Qy 99 AspProTrpProAlaGIyProGIuProProGIuAsnProTrpProProAlaProGIuAl 118

Db 28174 GACCTTGCGCGGAGAGACCCGACCCCGAGAAACCCCTGGCTCTGCCCCCTGAGGTG 28115

Qy 119 AspAsnArgProGIuGIuGIuProAspIeuAspProProAlaArgGIuIuArg 136

Db 28114 GACAAACGACACTCAGAGAGAGCCAGCCTAAGCCACCCCGGAGAGATACGA 28061

RESULT 10

LOCUS AB023060

DEFINITION Homo sapiens genomic DNA, chromosome 6p21.3, HLA class I region,

ACCESSION AB023060

VERSION AB023060.1

KEYWORDS HTG.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS Shima,T., Tamiya,G., Oka,A., Takishima,N., Yamagata,T., Kikawa,E., Iwata,K., Tomizawa,M., Okaki,N., Kuwano,Y., Watanabe,K., Fukuzumi,Y., Itakura,S., Sugawara,C., Ono,A., Yamazaki,M., Tashiro,H., Ando,A., Ikemura,T., Soeda,E., Kimura,M., Bahram,S., and Inoko,H.

TITLE Molecular dynamics of MHC genesis unraveled by sequence analysis of the 1,796,938-bp HLA class I region

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (23), 13282-13287 (1999)

MEDLINE 20027539

PUBMED 10557312

REFERENCE 2 (bases 1 to 39196)

AUTHORS Shima,T. and Takishima,N.

TITLE Direct Submision

JOURNAL Submitted (29-JAN-1999) Takashi Shima, Tokai University School of Medicine, Kanagawa 259-1193, Japan

FEATURES

source

1..39196

/organism="Homo sapiens"

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Local Similarity: 100.00%
Query Match:    88.12%
DB:              9
                Gaps: 0
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                Matches: 118
                Conservative: 0
                Mismatches: 0
                Indels: 0
                Gaps: 0

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	ORIGIN	
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Pred. No.:	1,92e-19	Length: 39186
Score:	712.00	Matches: 118
Percent Similarity:	100.00%	Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0
Query Match: 88.12% Indels: 0
DB: 9 Gaps: 0
US-09-994-365-2 (1-136) x AB023060 (1-39196)

QY 19 GYIISerGlySerGlyGlyGlyHISProSerHISProProAlaGluuAParGluGluAla 38
DB 10634 GGCATCTCAGGCGAGCGAGGCGCAACCCCTCACCACCCAGAGGAGCGAGGAGCA 10693
QY 39 GlySerProThrLeuProGlnGlyProProValProGlyAPProTTPProGlyAlaPro 58
DB 10694 GGCCTCCCAACATGCTCTCAGGGGCGCCCGCCGCTCCCGGTACCTTGAGGCGGCGACCC 10753
QY 59 ProteuPheGluuAPProProProProThrArgProSerArgProTTPArgAPleuProGlu 78
DB 10754 CCTCTCTTAAGATCTCTCCGCTCAGCCCGCCGACGTCGTCGAGAGACCTGCTCGAA 10813
QY 79 ThrGlyValTTPProProGlnProProArgThrAPProProGlnProProArgProASP 98
DB 10814 ACTGAGTCTGGCCCTCGAAGCGCTGAGAACGGATCTCTCAACTCCCGGCGCTGAC 10873
QY 99 ASPProTTPProAlaGlyProGlnProProGluuAPProTTPProProAlaProGluVal 118
DB 10874 GACCCCTTGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 10933
QY 119 ASPAPArgProGlnGluuAPProAPleuAPProProArgGluGluTTPArg 136
DB 10934 GACACCCGACCTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 10987

RESULT 11
AC004195 40878 bp DNA linear PRI 08-DEC-1998
LOCUS DEPICTION Homo sapiens clone UMGCI:Y24C027 from 6p21, complete sequence.
AC004195
AC004195.1 GI:3980474
VERSION HTG.
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 40878)
Jener,M., Guillaudoux,T., Vu,Q., KutyaVin,T., Harter,H. and
Geraghty,D.B.

TITLE Large scale sequence analysis of the human MHC class I region
JOURNAL Unpublished (1998)
REMARK Fred Hutchinson Cancer Research Center
The Clinical Research Division
1100 Fairview Ave. N., P.O. Box 19024
Seattle, WA 98109-1024
Contact: Daniel E. Geraghty (geraghty@fhcrc.org)
2 (bases 1 to 40878)
Direct Submission
Submitted (23-FEB-1998) Human Genome Center, University of
Washington, Box 352145, Seattle, WA 98195, USA
3 (bases 1 to 40878)
Geraghty,D.E. and Olson,M.V.
Direct Submission
Submitted (08-DEC-1998) Human Genome Center, University of
Washington, Box 352145, Seattle, WA 98195, USA
University of Washington Human Genome Center
Box 352145 Seattle, WA 98195
Contact: Daniel E. Geraghty (geraghty@fhcrc.org)
On Dec 8, 1998 this sequence version replaced gi:2905865.
Overlapping Sequences:
5': UMGCI:Y14C057 (Genbank Accession: AC006047)
3': UMGCI:Y24C203

REFERENCE
AUTHORS
TITLE
JOURNAL
REMARK

COMMENT

Sequence Quality Assessment:
This entry has been annotated with sequence quality
estimates computed by the Phrap assembly program.
All manually edited bases have been reduced to quality zero.

Quality levels above 40 are expected to have less than
1 error in 10,000 bp.
Base-by-base quality values are not generally visible from the
Genbank flat file format but are available as part
of this entry's ASN.1 file.

Double stranded (DS) coverage: 77.6%
DS or two chemistry coverage: 100.0%
Single stranded regions: 0

Sequence Validation:

This sequence has been validated by Multiple Complete Digest
Mapping. Comparison of the experimentally derived map digest
fragments with sequence-predicted fragments is given below.
Small fragments below a variable cutoff (approximately 400-600bp)
are not mapped and hence do not appear in the table. There are no
significant remaining discrepancies between the experimental and
predicted values. Uniquely ordered fragment groups are separated
by dashed lines.

Map	BglII	Seq	HindIII	Seq	Map	NciI	Seq
5056.53	5005.00	979.90	957.00	8811.76	8685.00		
2289.48	2257.00	3644.92	3580.00	9333.67	9154.00		
5302.18	5207.00	5611.48	5525.00	814.06	801.00		
894.03	880.00	4618.79	4525.00	10116.87	9863.00		
3041.57	2999.00	1532.79	1530.00	2432.75	2413.00		
14697.70	14691.00	1726.25	1724.00				
		1479.40	1473.00				
		909.61	880.00				
		8223.42	7996.00				
		2404.83	2380.00				
		7342.43	7194.00				

FEATURES

Source

Location/Qualifiers
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/chromosome="6"
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/cell_line="CGM1"
/clone_lib="Wash U YAC Library"
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/rpt_family="Alu"
complement(4643..5052)
/rpt_family="Alu"
complement(5090..5149)
/rpt_family="MIR"
9346..9586
/rpt_family="Alu"
complement(9800..10094)
/rpt_family="Alu"
11553..11834
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12152..12410
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12650..13079
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repeat_region complement (15576, .15686)
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1571, .15969
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complement (17434, .17719)
repeat_region /rpc_family="Alu"
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complement (24760, .25051)
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complement (29340, .29635)
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30290, .30564
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30791, .31421
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repeat_region /rpc_family="Alu"
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repeat_region /rpc_family="Alu"
34426, .35134
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complement (35292, .35444)
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complement (40436, .40717)
repeat_region /rpc_family="Alu"
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Pred. No.: 1,98e-19 Length: 40878
Score: 712.00 Matches: 118
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 88.12% Indels: 0
DB: 9 Gaps: 0
US-09-994-365-2 (1-136) x AC004195 (1-40878)
QY 19 GlyT1SerGlySerGluGlyHisProSerHisProProAlaGluAspArgGluGluAla 38
DB 27088 GGCACTTCACAGCAGCGAGGCGACCCCTCTACCCACCGCAGAGGACCGAGAGGAGCA 27147
QY 39 GlySerProThrLeuProGlnGlyProProValProGlyAspProTyrProGlyAlaPro 58
DB 27148 GGCTCCCAACATTTGCTCAGGGGCCCCCAAGTCCCGGTGACCTTGGCCAGGGGCA 27207
QY 59 ProLeuPheGluAspProProProThrArgProSerArgProTyrArgAspLeuProGlu 78
DB 27208 CCTCTTTGAAGATCTCTCCGCTACCCGCGCCAGTGTCTCTGAGAGAGACTGCTGAA 27267

QY 79 ThrGlyValTyrProProGluProProArgThrAspProProGluProProArgProAsp 98
DB 27268 ACTGAGAGTCTGGCCCCCTGACCGCCTAGAGGAGATCTCTCAACTCCCGGGCTGAC 27327
QY 99 AspProTyrProAlaGlyProGlnProProGluAsnProTyrProProAlaProGluVal 118
DB 27328 GACCTTTGGCCGCGACAGACCCCGCCAGAAACCTTGGCTCTGCTCCCTGAGGTG 27387
QY 119 AspAsnArgProGlnGluProAspLeuAspProProArgGluGluTyrArg 136
DB 27388 GACACCGAAGCTTACAGAGAGGACCACTTAGACCCCGGAGAGAGTACAGA 27441
RESULT 12
LOCUS AX522117 55050 bp DNA linear PAT 24-OCT-2002
DEFINITION Sequence 4 from Patent WO02064831.
ACCESSION AX522117
VERSION AX522117.1 GI:24411002
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Lench,N.J., Allen,M.J. and Nicholas,R.K.
TITLE Test and model for inflammatory disease
JOURNAL Patient: WO 02064831-A 4 22-AUG-2002;
Oxygen Limited (GB)
FEATURES
Location/Qualifiers
source 1..55050
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
ALIGNMENT SCORES:
Pred. No.: 2.45e-19 Length: 55050
Score: 712.00 Matches: 118
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 88.12% Indels: 0
DB: 6 Gaps: 0
US-09-994-365-2 (1-136) x AX522117 (1-55050)
QY 19 GlyT1SerGlySerGluGlyHisProSerHisProProAlaGluAspArgGluGluAla 38
DB 27099 GGCACTTCACAGCAGCGAGGCGACCCCTCTACCCACCGCAGAGGACCGAGAGGAGCA 27158
QY 39 GlySerProThrLeuProGlnGlyProProValProGlyAspProTyrProGlyAlaPro 58
DB 27159 GGCTCCCAACATTTGCTCAGGGGCCCCCAAGTCCCGGTGACCTTGGCCAGGGGCA 27218
QY 59 ProLeuPheGluAspProProProThrArgProSerArgProTyrArgAspLeuProGlu 78
DB 27219 CCTCTTTGAAGATCTCTCCGCTACCCGCGCCAGTGTCTCTGAGAGAGACTGCTGAA 27278
QY 79 ThrGlyValTyrProProGluProProArgThrAspProProGlnProProArgProAsp 98
DB 27279 ACTGAGAGTCTGGCCCCCTGACCGCCTTAGAACGATCTCTCAACTCCCGGGCTGAC 27338
QY 99 AspProTyrProAlaGlyProGlnProProGluAsnProTyrProProAlaProGluVal 118
DB 27339 GACCTTTGGCCGCGACAGACCCCGCCAGAAACCTTGGCTCTGCTCCCTGAGGTG 27398
QY 119 AspAsnArgProGlnGluProAspLeuAspProProArgGluGluTyrArg 136
DB 27399 GACACCGAAGCTTACAGAGAGGACCACTTAGACCCCGGAGAGAGTACAGA 27452
RESULT 13
LOCUS AL662867 70288 bp DNA linear PRI 24-APR-2002

DEFINITION	Human DNA sequence from clone Xxbac-34D1 on chromosome 6, complete sequence.
ACCESSION	AL662867
VERSION	AL662867.5
KEYWORDS	GI:20068664
SOURCE	HTG.
ORGANISM	Homo sapiens (human)
REFERENCE	Homo sapiens
AUTHORS	Eukaryotes, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
TITLE	1
JOURNAL	Sycamore, N.
COMMENT	Direct submission Submitted (22-APR-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: clonerequest@sanger.ac.uk hangquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Apr 7, 2002 this sequence version replaced gi:19309560. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above. This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em, EMBL; Sw, SWISSPROT; Tr, TREMBL; Wp, WORMPEP; information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep Xxbac-34D1 is from a CHORI-502 human bac - COX cell line library VECTOR: pTARBAC2.1 This sequence was generated from part of bacterial clone contigs constructed by the MHC HaploType Consortium and collaborators. Further information can be found at http://www.sanger.ac.uk/HGP/chrf/MHC .
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	/db_xref="taxon:9606"
	/chromosome="6"
	/clone="Xxbac-34D1"
	/clone_1kb="CHORI-502"
ORIGIN	
Alignment Scores:	2.91e-19
Pred. No.:	70288
Score:	712.00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	88.12%
DB:	Gaps: 0
US-09-394-365-2 (1-136) x AL662867 (1-70288)	
QY	19 G1Y11SeerGlySerGluGluYH1aPProSeH1aPProAlaGluAmpArgGluGluA1a 38
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QY	39 G1YSePrProH1eupProG1nG1YProProVa1ProG1YAppProTrppProG1YAlaPro 58
Db	67663 GGCCTCCCAACATTGCTTCAGAGGCCGCCCAAGTCTCCCGGTACCTTTGGCCAGGGGGACCC 67604
QY	59 ProLeuBheG1uAAppProProTrH1aYProSeH1aYProTrH1aYAppLeuProG1u 78
Db	67603 CCTCTCTTTGAAGATCTCTCGGCGTACCGGCCGCGAGTGTCCCTGAGAGAGACCTGGCTGAA 67544
QY	79 Th1eYAlaTrppProProG1uProProAlaYTh1aYAppProProG1uProProAlaYTrpp 98

Db	67543	ACTGSAATCTGGCCCCCTGAACCGGCTTAGACGATCTCTCAACTCCCGGCTGAC	67488
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Db	67483	GACCTTGCGCGGAGGACCCGACCCCGAAGAAACCCCTGGCTCTGCTCGCTGAGG	67422
Oy	119	AspAsnArgProGlnGluGluProAlaPheLeuAspProProArgGluGluTyrArg	136
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RESULT 14			
AP000510			
LOCUS			
DEFINITION	AP000510	99999 bp DNA linear	PRI 22-AUG-2001
ACCESSION		Homo sapiens genomic DNA, chromosome 6p21.3, HLA Class I region,	
VERSION		section 9/20.	
KEYWORDS		AP000510 BA000025	
SOURCE		AP000510.2 GI:7380878	
ORGANISM		Homo sapiens (human)	
REFERENCE		Homo sapiens	
AUTHORS		Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
JOURNAL		Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
REFERENCE		1	
AUTHORS		Shima, S., Tamiya, G., Oka, A. and Inoko, H.	
JOURNAL		Homo sapiens 2,725,817bp genomic DNA of 6p21.3 HLA class I region	
REFERENCE		Published Only in Database (1999)	
AUTHORS		2 (bases 1 to 99999)	
TITLE		Hirakawa, M., Yamaguchi, H., Imai, K. and Shimada, J.	
JOURNAL		Submitted (21-SEP-1999) Mike Hirakawa, Japan Science and Technology	
		Corporation (JST), Advanced Databases Department, 5-3, Yonbancho,	
		Chiyoda-ku, Tokyo 102-0081, Japan (E-mail: mlka@okyo.jst.go.jp),	
		URL: http://www-alis.tokyo.jst.go.jp/, Tel: 81-3-5214-8491,	
		Fax: 81-3-5214-8470	
COMMENT		On Mar 31, 2000 this sequence version replaced gi:5926697.	
		This sequence is conducted by Tokai University as a JST sequencing	
		Team.	
		Principal Investigator: Hidetoshi Inoko Ph.D	
		Phone: +81-463-93-1121, Fax: +81-463-94-8884,	
		The sequence is submitted by Human Genome Sequencing in AIS	
		project of JST	
		Japan Science and Technology Corporation (JST)	
		5-3, Yonbancho, Chiyoda-ku, Tokyo, 102-0081 Japan	
		For further information about this sequences, please visit our	
		sequence archive Web site (http://www-alis.tokyo.jst.go.jp/HGS/top.	
		html) or send email to webmaster@www-alis.tokyo.jst.go.jp	
		Sequence updated (28-Mar-2000).	
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		/map="6p21.3"	
		2016..2435	
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exon		2016..2435	
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		/number=6	
gene		complement(join(2144..2435,3297..3319))	
		/gene="SSEK1"	
		complement(join(2144..2435,3297..3319))	
CDS		/gene="SSEK1"	
		/codon_start=1	
		/protein_id="BAB6314.1"	
		/db_xref="GI:15277221"	
		/translation="MEPANHFMHAGDLQAMISKREHFLATODDCRKGRTQEDILVSS	
		HEPLTFASVLPMAPEEARLQOPLPPEGGIHLASRTLAFTLTYSSPPSHSPFGILS	
		LI"	
gene		join(2735..3104,3770..4542)	
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Alignment Scores:	
Pred. No.:	3,74e-19
Score:	712.00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	88.12%
DB:	9
	Gaps: 0
	Indels: 0
	Mismatches: 0
	Conservative: 0
	Matches: 118
	Length: 99999

US-09-994-365-2 (1-136) x AP000510 (1-999999)

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em: EMBL; Sw: SWISSPROT; Tr: TREMBL; Wp: WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs constructed by the MHC HaploType Consortium and collaborators. Further information can be found at <http://www.sanger.ac.uk/HGP/Chr6/MHC>

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_p2n model

Run on: January 11, 2005, 11:40:34 ; Search time 2821.18 Seconds
(without alignments)
1756.640 Million cell updates/sec

Title: US-09-994-365-2
Perfect score: 808
Sequence: 1 MIMMWKLGLIVLCLHTRGI.....EVDNRQEPEDLDLPREYR 136

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 32822875 seqs, 18219865908 residues
Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODE=frame+ p2n.model -DEV=x1h
-Q/cgn2_1/USPTO.spool_h/US0994365/runat_10012005_172232_6834/app.query.fasta_1.590
-DB=EST -QPMT=faetap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0
-UNITS-bits -START=1 -END=1 -MATRIX-blosum62 -TRANS=human40.cdi -LIST=45
-DOCCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US0994365 @CNC 1.1.4385 @runat_10012005_172232_6834 -NCPU=6 -ICPU=3
-NO MAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSBLOC=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST: *
1: gb_esc1: *
2: gb_esc2: *
3: gb_esc3: *
4: gb_esc4: *
5: gb_esc5: *
6: gb_esc6: *
7: gb_esc7: *
8: gb_esc8: *
9: gb_esc9: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	646	80.0	634	7	CF764947 CEST003088
2	619	76.6	593	7	CF765720 CEST001471
3	617	76.4	383	2	AM315342 12593 MAR
4	536.5	66.4	422	1	AI596929 vj46e11.y
5	528.5	65.4	562	1	AA530301
6	510.5	63.2	451	9	AA530301 vj46e11.y
7	507	62.7	416	9	CG484009 OST17807
8	506	62.6	669	9	CG481452 OST13885
9	501	62.0	442	9	CG484609 OST18617
					CG487403 OST22893

10	471.5	58.4	475	9	CG473878
11	460	56.9	322	9	CG474695
12	446.5	55.3	332	1	AA763309
13	441	54.6	386	1	CG474680
14	425	52.6	451	1	AA798896
15	375	46.4	355	9	CG528207
16	363	44.9	283	8	CG474588 OST2599 M
17	345	42.7	243	8	AQ357151
18	298	36.9	204	1	AA733661
19	283	35.0	379	1	AA791103
20	233	28.8	489	8	BH098389
21	209	25.9	984	4	BG441224
22	209	25.9	1380	9	CL058490
23	206	25.5	361	1	AA168568
24	205.5	25.4	812	9	AG133085
25	205.5	25.4	1218	9	AG435362
26	205	25.4	1272	9	AG365674
27	205	25.4	1283	9	AG435406
28	204.5	25.3	1585	8	CC294035
29	204.5	25.3	1691	9	AG341104
30	203.5	25.2	898	5	BQ411951
31	203.5	25.2	977	9	CL488066
32	203	25.1	848	9	CNS021YE
33	202.5	25.1	837	4	BG530104
34	202	25.0	1142	9	CL501710
35	202	25.0	1509	9	CL476587
36	201.5	24.9	688	8	AZ197670
37	201.5	24.9	666	8	BZ041090
38	201	24.9	1051	9	CL119109
39	201	24.9	2131	8	CC296269
40	200.5	24.8	628	6	CD890919
41	200.5	24.8	738	5	BQ805842
42	200.5	24.8	874	7	CK196627
43	200.5	24.8	1094	9	CC908599
44	200.5	24.8	1100	8	CC262597
45	200.5	24.8	1327	9	CL478195

ALIGNMENTS

RESULT 1
CF764947
LOCUS
DEFINITION CEST003088 Bos taurus skin cDNA library Bos taurus cDNA clone
CE1003088 5', mRNA sequence.

ACCESSION
CF764947
VERSION
CF764947.1 GI:37714166
KEYWORDS
EST.
SOURCE
Bos taurus (cow)
ORGANISM
Bos taurus

REFERENCE
Wang, Y.H., McWilliam, S. and Lehnert, S.
Transcription profiling of cattle skin
Unpublished (2003)
COMMENT
Contact: Dr Yonghong Wang
Functional Genomics Lab
CSIRO Livestock Industries
Level 5, Queensland Biosciences Precinct, University of Queensland,
306 Carmody Road St. Lucia QLD Australia
Tel: 07 3214 2445
Fax: 07 3214 2685
Email: Yonghong.Wang@csiro.au
Plate: 40 row: G column: 07.
location/Qualifiers

FEATURES
source
1..634
/organism="Bos taurus"
/mol_type="mRNA"
/strain="Hereford Shorthorn"
/db_xref="taxon:9913"
/clone="CTL003088"

JOURNAL
MEDLINE
PUBMED
COMMENT

Mamm. Genome 13 (8), 475-478 (2002)
22213789
12226715

Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390

Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and trimmed with phred
v0.960904.e. Vector identified by cross_match with the -minscore 20
and -mismatch 12 options.

PCR primers
FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTCCTCAGTCACGACG
Plate: 8 row: A column: 14
Seq primer: ATTAGCTGACACTATG.

FEATURES

source

1. 383

/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/tissue_type="pooled"
/lab_host="DHI0B"
/clone_lib="MARC 2P1G"
/note="Vector: PCMV SPORT6, Site 1: Not; Site 2: SalI;
library made from pooled tissue from testis, ovary,
endometrium, hypothalamus, pituitary, and placenta."

ORIGIN

Alignment Scores:

Pred. No.: 3,47e-29 Length: 383
Score: 617.00 Matches: 102
Percent Similarity: 85.83% Conservative: 7
Best Local Similarity: 80.31% Mismatches: 18
Query Match: 76.36% Indels: 0
DB: Gaps: 0

US-09-994-365-2 (1-136) x AM315342 (1-383)

QY 5 TTPVLSLEULEUGLYLEUVALLEUCYLSLEUHIETHRARGLYLIESERGLYSERGLU 24
DB 3 TGGAGAGCTACTGGGAGATCTGCTGCTTGGCTTCCCGAGGAGCATCTCAGACGCGGA 62
QY 25 GLYHISPROSETHISPROFROALAGUASPARGLUGLUALAGYSEPROTHIRLEU 44
DB 63 GACACCCCATCTCCCATCCACGAGGCGCTCAGAGGAGAGGAGGCGCTCCCAACATTGCT 122
QY 45 GLNGLYPROPROVALPROGLYASPPROTRTPROGLYVALPROFROLEUPHEGLUASPPRO 64
DB 123 CGGGGCCCCCATATCCCGGTGACCTTGGCGGAGGCTACTCTTATCTTGAAGACCT 182
QY 65 PROPROTHIRGPROSETHISPROTRTPARXASPLEUPROGLUITHIRGLYVALTTPROPRO 84
DB 183 CCAAGCTCCAGGCGCATCTGCTCGAGAGACCTGCTGAATCTGAGTCTGGCTCT 242
QY 85 GLUPROBROARGHTRASPPOPROGLINPROBROARGPROSPASPPROTRTPROALAGLY 104
DB 243 GAACCCCTTACTGATCTCCCTCAACCTCCCGGCTTACAGACCCCTGCGCAGCGGA 302
QY 105 PROGLINPROPROGLUASPPROTRTPROPROALAPROGLYVALASPAENATGPROGLINGLU 124
DB 303 CCCCAGCTCCAGAAAACCCCTGCGCAGCTGCTCGAGTGAAGTGAACACGAGATCCGAGAG 362
QY 125 GLUPROASPLEUASPPROPRO 131
DB 363 GAGCCAGACCTTGACCCAGCC 383

RESULT 4
LOCUS A1596929 422 bp mRNA linear EST 21-APR-1999
DEFINITION VJ46611.y1 StrataGene mouse skin (#937313) Mus musculus cDNA clone
IMAGE:932108 5', mRNA sequence.

ACCESSION A1596929
VERSION A1596929.1 GI:4605977
KEYWORDS EST.
SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 422)

Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wyllie, T.,
Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y.,
Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R.,
Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R.,
Waterson, R. and Wilson, R.

AUTHORS

The WashU-NCI Mouse EST Project 1999

TITLE

Unpublished (1999)

JOURNAL

CONTACT: Marra M/WashU-NCI Mouse EST Project 1999

COMMENT

Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.edu

This clone is available royalty-free through LML; contact the
IMAGE Consortium (info@image.lml.gov) for further information.
MWI:537028

This read is a RESSEQUENCE of a previously sequenced mouse clone
correct orientation)

Seq primer: -40RP from Gibco

High quality sequence stop: 396.

FEATURES

source

1. 422

/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:932108"
/sex="females"
/tissue_type="whole skin"
/dev_stage="11 weeks old"
/lab_host="SOLR (kanamycin resistant)"
/clone_lib="Stratagene mouse skin (#937313)"
/note="Organ: skin; Vector: pBluescript SK-; Site 1:
EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer:
Oligo dT. Whole skin from 11 week old C57BL/6 female mice.
Average insert size: 1.0 kb; Uni-ZAP XR Vector; -5'
adaptor sequence: 5' CTCGAGTCTTTTCTTTTCTTTT 3'."

ORIGIN

Alignment Scores:

Pred. No.: 3.62e-24 Length: 422
Score: 536.50 Matches: 89
Percent Similarity: 80.95% Conservative: 13
Best Local Similarity: 70.63% Mismatches: 23
Query Match: 66.40% Indels: 1
DB: Gaps: 1

US-09-994-365-2 (1-136) x A1596929 (1-422)

QY 11 LEUVALLEUCYLSLEUHIETHRARGLYLIESERGLYSERGLUHIHISPROSETHISPRO 30
DB 2 CTGCTCTTGGCTGTGTGTGAGAGGACATTTCAGCAAT---GGGACCTTTCTCCCGGA 58
QY 31 PROALAGLUASPARGLUGLUALAGYSEPROTHIRLEUPROGLINGLYPROPROVALPRO 50
DB 59 TCTACAGACACCCACAGAGGAGACTCCCACTGCTCTGAGGACCCCAATCCCT 118
QY 51 GLYASPPROTRTPROGLYVALPROFROLEUPHEGLUASPPROBROTHIRARGPROSER 70
DB 119 GGTGATCCCTGGGCGGCTCTCTTGTGTGAAGAACCTCGGCTCCAGGCTCCAC 178
QY 71 ARGPROTRPARASPLEUPROGLUITHIRGLYVALTTPROPROGLUUPROBROARGHTRASP 90

Db 179 CGTCCGTGAGAGATCTTCTGACAGTGTGCTGGCCCCCAAGCCCAAGCACTGAT 238

QY 91 ProProGlnProProAaPProAaPProTTPProAlaGlyProGlnProProGluAan 110
|||||
111

Db 239 CCCCCTAAACCTCTGCTGATGACCCCTGGCCAGCAAGCCCAAGCCCAAGAAAC 298
|||||

QY 111 ProTTPProProAlaProGluValaAaPnaAaPProGlnGluProAaPLeuAaPPro 130
|||||
299 CCGTGGCTCTCTGCTGCTGATGACCAATCATGAGAGAGAGCCAGCTTGACCA 358
|||||

QY 131 ProArgGluGluTyrArg 136
|||||
359 CCCCAGAGAGATATAGA 376
|||||

Db

RESULT 5
AA530301 562 bp mRNA linear EST 22-JUL-1997
LOCUS v146a11.r1 Stratagene mouse skin (#937313) Mus musculus cDNA clone
DEFINITION
AA530301
VERSION AA530301.1 GI:2273007
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM
REFERENCE
AUTHORS
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 562)
Marras, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellmberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lemmon, G., Soares, B., Wilson, R. and
Waterston, R.
The WashU-HMI Mouse EST Project
Unpublished (1996)
CONTACT: Marra M/Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LML; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:537028
Seq primer: -28ml3 rev1 ET from Amersham
High quality sequence stop: 221.
Location/Qualifiers
1. .562
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:932108"
/sex="females"
/tissue_type="whole skin"
/dev_stage="11 weeks old"
/lab_host="SOLR (kanamycin resistant)"
/clone_lib="Stratagene mouse skin (#937313)"
/note="Organ: skin; Vector: pBluescript SK-; Site: 1;
EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer:
Oligo dt. Whole skin from 11 week old C57BL/6 female mice.
Average insert size: 1.0 kb; Uni-ZAP XR Vector; ~5'
adaptor sequence: 5' GAATTCGGACGAG 3' ~3' adaptor
sequence: 5' CTCAGTTTCTTTTCTTTTCTTTT 3' "

ORIGIN
Alignment Scores:
Pred. No.: 1.53e-23 Length: 562
Score: 528.50 Matches: 88
Percent Similarity: 80.16% Conservative: 13
Best Local Similarity: 69.84% Mismatches: 24
Query Match: 65.41% Indels: 1
DB: 1 Gaps: 1

US-09-994-365-2 (1-136) x AA530301 (1-562)

QY 11 LeuValIleuCysLeuHisThrArgGlyIleSerGlySerGluGlyHisProSerHisPro 30
|||||
1 CTTGGTCTTTTGGCTGTGTGACAGAGGCACTTTCAGGCAAT--GGGACACCTCTTCCCGGA 57
|||||

Db 31 ProAlaGluAaPArgGluGluValaGlySerProThrLeuProGlnGlyProProValPro 50
|||||
58 TCACAGACACCAAGAAAGAGAGAGACTCCACCACTTCTCTGGGACCCCAATCCCT 117
|||||

QY 51 GlyAaPProTTPProGlyValaProProLeuPheGluAaPProProProThrArgProSer 70
|||||
118 GGTGATCCCTGGCTGGGCGGCTCTTTTGTGATGAACCTCCGCTCCAGCTCCAC 177
|||||

QY 71 ArgProTPArgAaPLeuProGluThrGlyValaTTPProProGluProProArgThrAaP 90
|||||
178 CGTCCGTGAGAGATTTCTCTGACAGTGTGCTGGCCCCCAAGCCCAAGCACTGAT 237
|||||

QY 91 ProProGlnProProAaPProAaPProTTPProAlaGlyProGlnProProGluAan 110
|||||
238 CCCCCTAAACCTCTGCTGATGACCCCTGGCCAGCAAGCCCAAGCCCAAGAAAC 297
|||||

QY 111 ProTTPProProAlaProGluValaAaPnaAaPProGlnGluProAaPLeuAaPPro 130
|||||
298 CCGTGGCTCTCTGCTGCTGATGACCAATCATGATTCAGAGAGAGCCAGACCTTGACCA 357
|||||

Db 131 ProArgGluGluTyrArg 136
|||||
358 ACCCAGAGAGATATAGA 375
|||||

QY

Db

RESULT 6
CG484009 451 bp DNA linear GSS 01-OCT-2003
LOCUS OST17807 Mus musculus 129Sv/Ev Mus musculus genomic clone OST17807,
DEFINITION
CG484009
VERSION CG484009.1 GI:37239343
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM
REFERENCE
AUTHORS
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 451)
Zambrowicz, B.P., Abuin, A., Ramirez-Solis, R., Richter, L.J.,
Piggett, J., BeltrandelRio, H., Buxton, E.C., Edwards, J., Finch, R.A.,
Riddle, C.J., Gupta, A., Hansen, G., Hu, Y., Huang, M., Jasing, C.,
Key, B.W., Jr., Kipp, P., Kohlhauff, B., Ma, Z.-O., Markesich, D.,
Payne, R., Pectter, D.G., Qian, N., Shaw, J., Schrick, J., Shi, Z.-Z.,
Sparks, M.J., Van Sligtenhorst, I., Vogel, P., Walke, W., Xu, N.,
Zhu, Q., Person, C. and Sands, A.T.
Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap
screen to identify potential targets for therapeutic intervention
Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
CONTACT: Zambrowicz BP
Omnibank
Lexicon Genetics Incorporated
4000 Research Forest Drive, The Woodlands, TX 77381, USA
Email: materials@lexgen.com
Gene trap sequence tag generated by 3' RACE from mouse ES cells as
described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
Class: Gene trap.
Location/Qualifiers
1. .451
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="129Sv/Ev"
/db_xref="taxon:10090"
/clone="OST17807"
/cell_type="embryonic stem cell"
/clone_lib="Mus musculus 129Sv/Ev"

ORIGIN

Alignment Scores:
Pred. No.: 1.57e-22 Length: 451
Score: 510.50 Matches: 83
Percent Similarity: 82.05% Conservatve: 13
Best Local Similarity: 70.94% Mismatches: 20
Query Match: 63.18% Indels: 1
Gaps: 1

US-09-994-365-2 (1-136) x CG484009 (1-451)

QY 20 TLESerGIySerGIyHISProSeRHiSPROAlaGIuAPArGIuGIuAlaGIy 39
Db 3 ATTTCAAGGCAAT---GGCGACCTTCTCCCGATCTACAGACACCAGAGAGAGAC 59
QY 40 SerProthLeuProGIuNGIyProProValProGIyAPProTPProGIyAlaProPro 59
Db 60 TCCCAACATTGGCTCTGGAGACCCCAATCTCTGTATCTCTGGCCCTGGGGCCCTCT 119
QY 60 LeuPheGIuAPProProProThArGPProSeArGPProTPArGAAPLeuProGIuThr 79
Db 120 TTGTTTATGAACCTCCGCCCTCCAGGCTCCAGCTCCCTGTGAGATCTTCTGACAGT 179
QY 80 GIyValTTPProGIuProProArGIuThArGPProGIuProProArGIuProArAP 99
Db 180 GATGCTGGCCCAAGACCCCAAGACATGATCCCTTAAACCTCTCTGATGAC 239
QY 100 ProTPProAlaGIyProGIuNGIyProProGIuAPProTPProProAlaProGIuAlaAP 119
Db 240 CCTGGGACAGAGAACCCCAAGAAACCTGGCTCTGCTGATGAGAC 299
QY 120 AsnArGPProGIuNGIyProAPLeuAPProProArGIuGIuTYrArg 136
Db 300 CATGAATCTCAAGAGAGACCACTTGAACCAACCAAGAGAGATAGA 350

RESULT 7
LOCUS CG481452 416 bp DNA linear GSS 01-OCT-2003
DEFINITION OST13885 Mus musculus 129Sv/Ev Mus musculus genomic clone OST13885,
genomic survey sequence.
ACCESSION CG481452
VERSION CG481452.1 GI:37233834
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 416)
Zambrowicz,B.P., Abuin,A., Ramirez-Solis,R., Richter,L.J.,
Piggott,J., Beltranderio,H., Buxton,B.C., Edwards,J., Finch,R.A.,
Fridde,C.J., Gupta,A., Hansen,G., Hu,Y., Huang,W., Jaiing,C.,
Key,B.W., Jr., Kipp,P., Kohlhauff,B., Ma,Z.-Q., Markesich,D.,
Payne,R., Potter,D.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.-Z.,
Spark,M.J., Van Sligtenhorst,I., Vogel,P., Walke,W., Xu,N.,
Zhu,Q., Person,C. and Sands,A.T.
Mkl kinase deficiency lowers blood pressure in mice: a gene-trap
screen to identify potential targets for therapeutic intervention
Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
CONTACT: Zambrowicz BP
OmniBank
Lexicon Genetics Incorporated
4000 Research Forest Drive, The Woodlands, TX 77381, USA
Email: materials@lexgen.com
Gene trap sequence tag generated by 3' RACE from mouse ES cells as
described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
Class: Gene Trap.

FEATURES
source 1..416
Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="129Sv/Ev"
/db_xref="taxon:10090"
/clone="OST13885"
/cell_type="embryonic stem cell"

ORIGIN /clone_1ib="Mus musculus 129Sv/Ev"

Alignment Scores:
Pred. No.: 2.37e-22 Length: 416
Score: 507.00 Matches: 80
Percent Similarity: 82.14% Conservatve: 12
Best Local Similarity: 71.43% Mismatches: 20
Query Match: 62.75% Indels: 0
Gaps: 0

US-09-994-365-2 (1-136) x CG481452 (1-416)

QY 25 GIyHISProSeRHiSPROAlaGIuAPArGIuGIuAlaGIySerProThLeuPro 44
Db 14 GGGACCTTCTTCCGATCTACAGACACCAGAGAGAGAGACTCCACCATTCCT 73
QY 45 GIuNGIyProProValProGIyAPProTPProGIyAlaProProLeuPheGIuAPPro 64
Db 74 CTGGAGACCCCAATCTCTGGATCTCTGGCTGGGGGCTCTCTTGTGTGAACCT 133
QY 65 ProProThArGPProSeArGPProTPArGAAPLeuProGIuThrGIyValTTPProPro 84
Db 134 CCGCTCTCAGAGCTCCACCTCTCTGAGAGATCTTCTTCAAGTGTGCTGCCCCCA 193
QY 85 GIuProProArGIuThArGPProGIuNGIyProProArGPProArAPProTPProAlaGIy 104
Db 194 AAGCCCCAGACTATCTCCCTTAACTCTCTGTATGACCTTGGCCAGAGAG 253
QY 105 ProGIuProProGIuAPProTPProProAlaProGIuAlaAPArAPProGIuNGIy 124
Db 254 ACCAGCCCCAGAAACCTCTGGCTCTGCTCTGATGAGCATGATCTCAGAG 313
QY 125 GIuProAPLeuAPProProArGIuGIuTYrArg 136
Db 314 GAGCGAGACCTTGAACCAACCAAGAGAGATAGA 349

RESULT 8
LOCUS CG484609 669 bp DNA linear GSS 01-OCT-2003
DEFINITION OST18617 Mus musculus 129Sv/Ev Mus musculus genomic clone OST18617,
genomic survey sequence.
ACCESSION CG484609
VERSION CG484609.1 GI:37240590
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 669)
Zambrowicz,B.P., Abuin,A., Ramirez-Solis,R., Richter,L.J.,
Piggott,J., Beltranderio,H., Buxton,B.C., Edwards,J., Finch,R.A.,
Fridde,C.J., Gupta,A., Hansen,G., Hu,Y., Huang,W., Jaiing,C.,
Key,B.W., Jr., Kipp,P., Kohlhauff,B., Ma,Z.-Q., Markesich,D.,
Payne,R., Potter,D.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.-Z.,
Spark,M.J., Van Sligtenhorst,I., Vogel,P., Walke,W., Xu,N.,
Zhu,Q., Person,C. and Sands,A.T.
Mkl kinase deficiency lowers blood pressure in mice: a gene-trap
screen to identify potential targets for therapeutic intervention
Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
CONTACT: Zambrowicz BP
OmniBank
Lexicon Genetics Incorporated
4000 Research Forest Drive, The Woodlands, TX 77381, USA
Email: materials@lexgen.com
Gene trap sequence tag generated by 3' RACE from mouse ES cells as
described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
Class: Gene Trap.

FEATURES
source 1..669
Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="129Sv/Ev"

Class: Gene Trap.
Location/Qualifiers
1. .475
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="129Sv/Ev"
/db_xref="taxon:10090"
/clone="OST1668"
/cell_type="embryonic stem cell"
/clone_lib="Mus musculus 129Sv/Ev"

ORIGIN

Alignment Scores:
Pred. No.: 4,25e-20 Length: 475
Score: 471.50 Matches: 74
Percent Similarity: 80.37% Conservative: 12
Best Local Similarity: 69.16% Mismatches: 16
Query Match: 58.35% Indels: 5
DB: 9 Gaps: 1

US-09-994-365-2 (1-136) x CG473878 (1-475)

Qy 29 HisProProAlaGluAspArgGluGluAlaGlySerProThrLeuProGlnGlyProPro 48
Db 40 CACCCA-----CGAAAGAGAGATCCCAACCATTCCTGCGACCCCA 84

Qy 49 ValProGlyAspProTyrProGlyAlaProProLeuPheGluAspProProProThrArg 68
Db 85 ATCCCTGATGATCCCTGAGCTGAGGAGCGCTCTGTGTGTAAGAACCTCCGCTCCAGGC 144

Qy 69 ProSerArgProTyrAspLeuProGluThrGlyValTyrProProGluProProArg 88
Db 145 TCCACACGCTCCCTGAGAGATCTTCTGACAGTGTGCTGCTGCCCCCAAGCCCCCAAGC 204

Qy 89 ThrAspProProGlnProProArgProAspAspProTyrProAlaGlyProGlnProPro 108
Db 205 ACTGATCCCTCTAAACCTCTCTGCTGATGACCTGCGCAGAGAACCCAGCCCCCA 264

Qy 109 GluAsnProTyrProProAlaProGluValAspAsnArgProGlnGluGluProAspLeu 128
Db 265 NAAAGCCCTGAGCTCTGCGCCCTGAAATGAGCAGTAACTCAGAGAGACCCAAACTT 324

Qy 129 AspProProArgGluGluTyr 135
Db 325 GACCCACCCCAAGAAANTAT 345

RESULT 11
CG474695 322 bp DNA linear GSS 01-OCT-2003
LOCUS OST2738 Mus musculus 129Sv/Ev Mus musculus genomic clone OST2738,
DEFINITION genomic survey sequence.
ACCESSION CG474695
VERSION CG474695.1 GI:37225584
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 322)
REFERENCE Zambronicz, B.P., Abuin, A., Ramirez-Solis, R., Richter, L., J.,
Pigot, C.J., Gupta, A., Hansen, G., Hu, Y., Huang, W., Jais, R.A.,
Key, B.W., Jr., Kipp, P., Kohlhauff, B., Ma, Z.-Q., Markesich, D.,
Payne, R., Potter, D.G., Qian, N., Shaw, J., Schrick, J., Shi, Z.-Z.,
Spark, M.J., Van Sligtenhorst, I., Vogel, P., Walke, W., Xu, N.,
Zhu, Q., Person, C. and Sands, A.T.
Wnt1 kinase deficiency lowers blood pressure in mice: a gene-trap
screen to identify potential targets for therapeutic intervention
Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
CONTACT: Zambronicz BP
OMIBANK
Lexicon Genetics Incorporated
4000 Research Forest Drive, The Woodlands, TX 77381, USA

Email: material@lexgen.com
Gene trap sequence tag generated by 3' RACE from mouse ES cells as
described in Zambronicz et al (Nature, 1998 Apr 9;392(6676):608-11)
Class: Gene Trap.
Location/Qualifiers
1. .322
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="129Sv/Ev"
/db_xref="taxon:10090"
/clone="OST2738"
/cell_type="embryonic stem cell"
/clone_lib="Mus musculus 129Sv/Ev"

ORIGIN

Alignment Scores:
Pred. No.: 1,45e-19 Length: 322
Score: 460.00 Matches: 74
Percent Similarity: 82.35% Conservative: 10
Best Local Similarity: 72.55% Mismatches: 17
Query Match: 56.93% Indels: 1
DB: 9 Gaps: 0

US-09-994-365-2 (1-136) x CG474695 (1-322)

Qy 36 GluGluAlaGlySerProThrLeuProGlnGlyProProValProGlyAspProTyrPro 55
Db 6 AAGAGAGAGACTCCCAACCATTCCTGAGACCCCAATCCCTGTGATCCCTGAGCT 65

Qy 56 GlyAlaProProLeuPheGluAspProProProThrArgProSerArgProTyrArgAsp 75
Db 66 GGGGCGCTCTCTTTGTTGTAAGACCTCCGCTCAGAGCTCAACCGTCCCTGAGAGAT 125

Qy 76 LeuProGluThrGlyValTyrProProGluProProArgTyrThrAspProProGlnProPro 95
Db 126 CTTCCTACACTGTGTGCTGCGCCCAAGAGCCCAAGCACTGATCCCTTAACCTCT 185

Qy 96 ArgProAspAspProTyrProAlaGlyProGlnProProGluAsnProTyrProProAla 115
Db 186 CTGCTGATGACCTCCCTGAGCAGAGAACCCCAAGAACCCCTGAGCTCTGCTCC 245

Qy 116 ProGluValAspAsnArgProGlnGluGluProAspLeuAspProProArgGluGluTyr 135
Db 246 CTGAGATGAGCAGTAACTCAGAGAGAGCCAAACCTGACCCACCCAGGAAGATA 305

Qy 135 TAGT 136
Db 306 TAGA 309

RESULT 12
AA763309 332 bp mRNA linear EST 27-JAN-1998
LOCUS AA763309
DEFINITION v069h03.r1 Striatagene mouse skin (#537313) Mus musculus cDNA clone
IMAGE:1229621 5', mRNA sequence.
ACCESSION AA763309
VERSION AA763309.1 GI:2813056
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 332)
REFERENCE Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisler, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theisinger, B., Wyllie, T., Lennon, G., Soares, B., Wilson, R. and
Waterston, R.
The WashU-HMI Mouse EST Project
Unpublished (1996)
CONTACT: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@wustl.edu
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.lnl.gov) for further information.
 MGI:655213

Seq primer: -28ml3 rev1 ET from Amersham
 High quality sequence stop: 329.

FEATURES

source

1..332
 location/Qualifiers
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 /mol_type="mRNA"
 /strain="C57BL/6"
 /db_xref="taxon:10090"
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 /sex="females"
 /tissue_type="whole skin"
 /dev_stage="11 weeks old"
 /lab_host="SOLR (kanamycin resistant)"
 /clone_lib="Stratagene mouse skin (#937313)"
 /note="Organ: skin; Vector: phubscript SK-; Site: 1:
 EcoRI, Site 2: XhoI, Cloned unidirectionally. Primer:
 Oligo dt. Whole skin from 11 week old C57BL/6 female mice.
 Average insert size: 1.0 kb; Uni-ZAP XR Vector; ~5'
 adaptor sequence: 5' GAATTCGCGACGAG 3' ~3' adaptor
 sequence: 5' CTCGAGTTTCTTTTCTTTT 3' "

ORIGIN

Alignment Scores:

Pred. No.: 1.02e-18 Length: 332
 Score: 446.50 Matches: 77
 Percent Similarity: 81.48% Conservative: 11
 Best Local Similarity: 71.30% Mismatches: 15
 Query Match: 55.26% Indels: 7
 DB: 1 Gaps: 1

US-09-994-365-2 (1-136) x AA763309 (1-332)

Qy 29 HisProProAlaGluAspArgGluGluAlaGlySerProThrLeuProGlnGlyProPro 48
 Db 3 CACCCA-----CGAAGAGAGAGACTCCACCATTCCTCTGAGACCCCA 47
 Qy 49 ValProGlyAspProTrrProGlyAlaProProLeuPheGluAspProProProThyArg 68
 Db 48 ATCCCTGGTGAATCCCTGGCTGGGGG-CCTCCTTTGTTGATGAACCTCCGCTCC-AGG 105
 Qy 69 ProSerArgProTrrPArgAspLeuProGluThrglyValTrrProProGluProProArg 88
 Db 106 TCCAAACCTCCCTGGAGAGATCTTCGACAGTGGTGCCTGGCCCCCAAAAGCCCCCAAGC 165
 Qy 89 ThrAspProProGlnProProArgProAspAspProTrrProAlaGlyProGlnProPro 108
 Db 166 ACTGATCCCCCTAAACCTCTCTGCTGATATGACCTCGCCAGCAGAAACCCAGCCCCCA 225
 Qy 109 GluAsnProTrrProProAlaProGluValAspAsnArgProGlnGluGluProAspLeu 128
 Db 226 GAAACCCCTGGCTCCCTGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 285
 Qy 129 AspProProArgGluGluTrrArg 136
 Db 286 GACCCACCCCGAGAGAGATATAGA 309

RESULT 13

CG474680

LOCUS CG474680 386 bp DNA linear GSS 01-OCT-2003
 DEFINITION OST2720 Mus musculus 129Sv/Ev Mus musculus genomic clone OST2720,
 genomic survey sequence.

ACCESSION

CG474680

VERSION CG474680.1 GI:37225569

KEYWORDS

GSS. Mus musculus (house mouse)

SOURCE

Mus musculus (house mouse); Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

REFERENCE

1 (bases 1 to 386)
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AUTHORS

Zambowicz, B.P., Abuin, A., Ramirez-Solis, R., Richter, L.J.,
 Piggett, J., Beltrander, R.H., Buxton, E.C., Edwards, J., Finch, R.A.,
 Fridde, C.J., Gupta, A., Hansen, G., Hu, Y., Huang, W., Jiang, C.,
 Key, B.W., Jr., Kipp, P., Kohlhauf, B., Ma, Z.-Q., Markesich, D.,
 Payne, R., Potter, D.G., Qian, N., Shaw, J., Schlick, J., Shi, Z.-Z.,
 Sparks, M.J., Van Sighemore, I., Vogel, P., Walke, W., Xu, N.,
 Zhu, Q., Person, C. and Sands, A.T.
 Wk1 kinase deficiency lowers blood pressure in mice: a gene-trap
 screen to identify potential targets for therapeutic intervention
 Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
 Contact: Zambowicz BP

TITLE

JOURNAL

COMMENT

OmniBank
 Lexicon Genetics Incorporated
 4000 Research Forest Drive, The Woodlands, TX 77381, USA
 Email: materials@lexgen.com
 Gene trap sequence tag generated by 3' RACE from mouse ES cells as
 described in Zambowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
 Class: Gene Trap.

FEATURES

source

1..386
 location/Qualifiers
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 /mol_type="genomic DNA"
 /strain="129Sv/Ev"
 /db_xref="taxon:10090"
 /clone="OST2720"
 /cell_type="embryonic stem cell"
 /clone_lib="Mus musculus 129Sv/Ev"

ORIGIN

Alignment Scores:

Pred. No.: 2.61e-18 Length: 386
 Score: 441.00 Matches: 68
 Percent Similarity: 75.45% Conservative: 15
 Best Local Similarity: 61.82% Mismatches: 27
 Query Match: 54.58% Indels: 0
 DB: 9 Gaps: 0

US-09-994-365-2 (1-136) x CG474680 (1-386)

Qy 27 ProSerHisProProAlaGluAspArgGluGluAlaGlySerProThrLeuProGlnGly 46
 Db 7 CTTCTCCCGATCTACAGACACCACCAAGAGAGACTCCACCATTCCTCTGGGA 66
 Qy 47 ProProValProGlyAspProTrrProGlyAlaProProLeuPheGluAspProProPro 66
 Db 67 CCCCCAATCCCTGATGATCCCTGGCTGGGGGCGCTCTTTGTTGATGATGATGATGATGAT 126
 Qy 67 ThrArgProSerArgProTrrPArgAspLeuProGluThrglyValTrrProProGluPro 86
 Db 127 CAGAGCTCAACCGTCCCTGGANAGATCTCTGACANTGAGTGGCTGGCCCCCAAGCCC 186
 Qy 87 ProArgThrAspProProGlnProProArgProAspAspProTrrProAlaGlyProGln 106
 Db 187 CNAAGNCATATCCCTCTAAACCTCTGCTGATATGATGATGATGATGATGATGATGATGAT 246
 Qy 107 ProProGluAsnProTrrProProAlaProGluValAspAsnArgProGlnGluGluPro 126
 Db 247 CCCCCAATAAACCCTGGCTCTGCGCCCTGGAATGAGATGAGATGAGATGAGATGAGATGAG 306
 Qy 127 AspLeuAspProProArgGluGluTrrArg 136
 Db 307 AACCTGACCCNCCCGAGAAATATATAA 336

RESULT 14

AA798896

LOCUS AA798896 451 bp mRNA linear EST 10-FEB-1998
 DEFINITION vv94e08.r1 Stratagene mouse skin (#937313) Mus musculus cDNA clone
 IMAGE:1230086 5', mRNA sequence.

ACCESSION

AA798896

VERSION AA798896.1 GI:2861851

KEYWORDS

EST.

SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 451)
AUTHORS Maier, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubouche, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Stepcoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.
TITLE The WashU-HMI Mouse EST Project
JOURNAL Unpublished (1996)
COMMENT Contact: Marra M/Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.edu
This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.lnl.gov) for further information.
MG1:655678
Putative full length read
vector to vector length is 671
Seq primer: -28m13 rev1 ET from Amersham
High quality sequence stop: 431.
Location/Qualifiers
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/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
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/sex="Female"
/tissue_type="whole skin"
/dev_stage="11 weeks old"
/lab_host="SOLR (kanamycin resistant)"
/clone_lib="Stratagene mouse skin (#93713)"
/note="Organ: skin; Vector: pBluescript SK-; Site_1: EcorI; Site_2: XhoI; Cloned unidirectionally. Primer: Oligo dt. Whole skin from 11 week old C57BL/6 female mice. Average insert size: 1.0 kb; Uni-ZAP XR Vector; ~5' adaptor sequence: 5' GAATTCGACGAG 3' ~3' adaptor sequence: 5' CTCGAGTTT TTT TTT TTT TTT 3'"

ORIGIN
Alignment Scores:
Pred. No.: 3e-17 Length: 451
Score: 425.00 Matches: 71
Percent Similarity: 89.01% Conservative: 10
Best Local Similarity: 78.02% Mismatches: 10
Query Match: 52.60% Indels: 2
DB: 1 Gaps: 0

US-09-994-365-2 (1-136) x AA798896 (1-451)

QY 46 G1yProProValPProG1yAaPPProTTPProG1yAlaPProPoleuPheGluAaPPProPro 65
DB 1 GGACCCCAACCTCTGGATCCCTGGCTGGGG-CCTCCTTTGTTTGAACCTCCG 59
QY 66 ProThArgProSerArgProTTPArgAspLeuPProGluThrGlyValTTPProProGlu 85
DB 60 CTCACAGCTCAAC-CGTCCCTGAGAGATCTTCTGACAGGTGCTGACCCCAAG 118
QY 86 ProProArgThArgProProGluInProProArgProAspAspProTTPProAlaGlyPro 105
DB 119 CCCCAGCACTGATCCCTCAACCTCTGCTGCTGATGACCCCTGCGCAGAGAAC 178
QY 106 G1nProProGluAaPPProTTPProProAlaPProGluValAaPAnaArgProGluGlu 125
DB 179 CAGCCCAAGAAACCCCTGGCTCTGCCCCCTGAGATGACCATGATCTCAGAGAG 238
QY 126 ProAspLeuAaPPProProArgGluGluTyrArg 136

DB 239 CCAGACCTTGACCAACCCAGAGAGATATGA 271
RESULT 15
LOCUS CG528207 395 bp DNA linear GSS 01-OCT-2003
DEFINITION OS1107284 Mus musculus 129SV/Bv Mus musculus genomic clone
ACCESSION CG528207
VERSION CG528207.1 GI:37314779
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 395)
AUTHORS Zambrowicz, B.P., Abuin, A., Ramirez-Solis, R., Richter, L.J., Piggott, J., Beltrande-Rio, H., Buxton, E.C., Edwards, J., Finch, R.A., Fridde, C.J., Gupta, A., Hansen, G., Hu, Y., Huang, W., Jaing, C., Key, B.W. Jr., Kipp, P., Kohlhauff, B., Ma, Z.-Q., Markesich, D., Payne, R., Potter, D.G., Qian, N., Shaw, J., Schrick, J., Shi, Z.-Z., Sparks, M.J., Van Sligtenhorst, I., Vogel, P., Walke, W., Xu, N., Zhu, Q., Person, C. and Sands, A.T.
TITLE Mkl kinase deficiency lowers blood pressure in mice: a gene-trap screen to identify potential targets for therapeutic intervention
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
COMMENT Contact: Zambrowicz BP
OmiBank
Lexicon Genetics Incorporated
4000 Research Forest Drive, The Woodlands, TX 77381, USA
Email: materials@lexgen.com
Gene trap sequence tag generated by 3' RACE from mouse ES cells as described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
Class: Gene trap.
Location/Qualifiers
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/organism="Mus musculus"
/mol_type="genomic DNA"
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/clone="OS1107284"
/cell_type="embryonic stem cell"
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ORIGIN
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Pred. No.: 3.2e-14 Length: 395
Score: 375.00 Matches: 63
Percent Similarity: 79.57% Conservative: 11
Best Local Similarity: 67.74% Mismatches: 17
Query Match: 46.41% Indels: 2
DB: 9 Gaps: 0

US-09-994-365-2 (1-136) x CG528207 (1-395)

QY 46 G1yProProValPProG1yAaPPProTTPProG1yAlaPProPoleuPheGluAaPPProPro 65
DB 3 GGACCCCAACCTCTGGATCCCTGGCTGGGG-CCTCCTTTGTTTGAACCTCCG 62
QY 65 oProThArgProSerArgProTTPArgAspLeuPProGluThrGlyValTTPProProGlu 85
DB 63 GCTTCAGGCTCAACACCTGCTGAGAGATNTTACGACAGTGTGCTGCCCCCAA 122
QY 85 uProProArgThArgProProGluInProProArgProAspAspProTTPProAlaGlyPro 105
DB 123 GCCCAAGCAGCATGCCCTCAACCTTCTGCTGATGACCCCTGCGCAGAGAAC 182
QY 105 roGluInProProGluAaPPProTTPProProAlaPProGluValAaPAnaArgProGluGlu 125
DB 183 CCGAGCCCAAGAAACCCCTGGCTCTGCCCCCTGAGATGACCATGATCTCAGAGAG 242
QY 125 lUpProAspLeuAaPPProProArgGluGluTyrArg 136

Thu Jan 13 09:19:07 2005

us-09-994-365-2.p2n.rst

Page 10

Db 243 AGCCAGACCTTGACCCACCCAGAGAGATATAGA 277

Search completed: January 11, 2005, 19:52:35
Job time : 2829.18 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: January 12, 2005, 16:40:28 ; Search time 83 Seconds
(without alignments)
976.264 Million cell updates/sec

Title: US-09-994-365-3

Perfect score: 692
Sequence: 1 SEGHPSHPAEDREAREAGSPR.....EVDNRQBPEDDLPPEEYR 114

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-LOOPEXT=0 -UNITS=b1ts -START=1 -END=-1 -MATRIX=bl0sum62 -TRANS=human40.cdl
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
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-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREDS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Issued Patents NA:*
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6: /cgn2_6/prodata/1/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	304.5	44.0	248	US-09-621-976-9776	Sequence 9776, Ap
C 2	198.5	28.7	4403765	US-09-103-840A-1	Sequence 2, Appli
C 3	198.5	28.7	4411529	US-09-103-840A-1	Sequence 1, Appli
C 4	190.5	27.5	1926	US-09-249-585A-4	Sequence 4, Appli
C 5	190.5	27.5	1931	US-09-130-114-2	Sequence 4, Appli
C 6	188.5	27.2	4403765	US-09-103-840A-2	Sequence 2, Appli
C 7	188.5	27.2	4403765	US-09-103-840A-2	Sequence 2, Appli
C 8	182	26.3	114793	US-10-148-806-3	Sequence 3, Appli
C 9	181	26.2	6530	US-08-146-930-1	Sequence 1, Appli
C 10	181	26.2	6530	US-08-458-240-1	Sequence 1, Appli
C 11	181	26.2	6530	PCT-US93-03993-1	Sequence 1, Appli
C 12	180.5	26.1	1854	US-09-894-844-103	Sequence 103, App

C 13	180	26.0	1280	3	US-09-060-756-4	Sequence 4, Appli
C 14	180	26.0	1280	4	US-09-670-314-4	Sequence 4, Appli
C 15	179.5	25.9	152331	3	US-09-128-155-16	Sequence 16, Appli
C 16	176	25.4	320	3	US-09-165-264-14	Sequence 14, Appli
C 17	174.5	25.2	2830	2	US-09-010-928B-1	Sequence 1, Appli
C 18	171.5	24.8	1173	4	US-09-894-844-60	Sequence 60, Appli
C 19	171	24.7	320	3	US-09-165-264-7	Sequence 7, Appli
C 20	171	24.7	320	3	US-09-165-264-11	Sequence 11, Appli
C 21	171	24.7	1926	4	US-09-249-585A-2	Sequence 2, Appli
C 22	171	24.7	1926	4	US-09-410-399-3	Sequence 3, Appli
C 23	171	24.7	2580	3	US-09-050-863-2	Sequence 2, Appli
C 24	171	24.7	2580	3	US-09-359-081-2	Sequence 2, Appli
C 25	171	24.7	5452	2	US-09-130-114-1	Sequence 1, Appli
C 26	171	24.7	8705	4	US-09-647-344A-14	Sequence 14, Appli
C 27	171	24.7	9600	3	US-08-910-647-1	Sequence 1, Appli
C 28	171	24.7	9600	4	US-09-620-925-1	Sequence 1, Appli
C 29	171	24.7	10596	1	US-07-884-811-15	Sequence 15, Appli
C 30	171	24.7	10596	1	US-07-885-971-15	Sequence 15, Appli
C 31	171	24.7	10596	1	US-08-087-783A-15	Sequence 15, Appli
C 32	171	24.7	10596	1	US-08-194-088B-15	Sequence 15, Appli
C 33	171	24.7	10596	2	US-08-194-087-15	Sequence 15, Appli
C 34	171	24.7	10596	5	PCT-US93-04648-15	Sequence 15, Appli
C 35	171	24.7	16080	4	US-09-724-566A-48	Sequence 48, Appli
C 36	170	24.6	318	3	US-09-165-264-13	Sequence 13, Appli
C 37	169.5	24.5	320	3	US-09-165-264-12	Sequence 12, Appli
C 38	169	24.4	290	3	US-08-818-112-37	Sequence 37, Appli
C 39	169	24.4	290	3	US-08-818-112-37	Sequence 37, Appli
C 40	169	24.4	290	3	US-09-056-556-37	Sequence 37, Appli
C 41	169	24.4	290	4	US-09-072-596-37	Sequence 37, Appli
C 42	169	24.4	290	4	US-09-072-597-37	Sequence 37, Appli
C 43	168.5	24.3	1548	2	US-08-762-106-5	Sequence 5, Appli
C 44	168.5	24.3	1548	3	US-09-320-774-5	Sequence 5, Appli
C 45	168.5	24.3	1581	2	US-08-762-106-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1
US-09-621-976-9776/c
Sequence 9776, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas MLine Edwards, J.B.
APPLICANT: Jobert, S.
TITLE OR INVENTION: ESTs and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 9776
LENGTH: 248
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: 188
OTHER INFORMATION: n=a, g, c or t
US-09-621-976-9776

Alignment Scores:

Pred. No.: 7 25e-13
Score: 304.50
Percent Similarity: 88.33%
Best Local Similarity: 86.67%
Query Match: 44.00%
DB: 4
Gaps: 1
US-09-994-365-3 (1-114) x US-09-621-976-9776 (1-248)

QY 56 G|U|T|h|G|y|V|a|l|T|r|P|P|r|o|G|u|P|r|o|G|a|T|T|h|A|S|P|r|o|G|u|P|r|o|G|a|T|G|P|r|o 75
|||||

Db 184 GAAACTGAGTCTGCGCCCTGAAACGCGCTAGAACGAGTCTCTCAACTCCCGGCGCT 125
Qy 76 AaAaPProTTPProAlaGlyProGlnProGlu---AaProTTPProAlaPro 94
Db 124 GACGACCCCTTGGCGCGGAGAGACCCCGCCGAGAAACCCCTGCTCTGCGCT 65
Qy 95 GluValAaAaPProGlnGluGluProAaPleuAaPProProAlaGluGluTyrArg 114
Db 64 GAGGTGACAAACGACCTCAGAGAGAGCCAGACTTACACCCCGGAGAGACTACGA 5

RESULT 2
US-09-103-840A-2/c
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; FILE REFERENCE: 24366-2007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

Alignment Scores:
Pred. No.: 0.143 Length: 4403765
Score: 198.50 Matches: 51
Percent Similarity: 32.54% Conservative: 4
Best Local Similarity: 30.18% Mismatches: 45
Query Match: 28.68% Indels: 69
DB: 3 Gaps: 6

US-09-994-365-3 (1-114) x US-09-103-840A-2 (1-4403765)

Qy 5 ProSerHisProProAlaGluAaPArgGluGluAaGlySerProThrLeuProGlnGly 24
Db 1091482 CCGCCGATGCGCGCGCGCGCGCGCTCCGCGCGCGCTCGCGCGCGCGCGCAACGCG 1091423
Qy 25 ProProValProGlyAaPProTTPProGlyAlaProProLeuPheGluAaPPro----- 42
Db 1091422 CCACTACCGCGCGCGCGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTG 1091363
Qy 43 -----ProProThrArgProSerArg 49
Db 1091362 CCGCGCATCCCAACCGCGCGCAACCGATCCCGCGCGCGCGCGCGCGCGCGCGCGCG 1091303
Qy 50 ProTTP-----ArgAaPleuPro 55
Db 1091302 CCGTGGCGCGCTGCTCAACCATGCGCGATGCGCTCAAGCGCGCGCGCGCGCGCTGCG 1091243
Qy 56 GluThrGlyValTTPProProGluProProArgThraP----- 68
Db 1091242 CCAAGACCGCGCTGCG 1091183
Qy 69 -----ProProGlnPro 72
Db 1091182 CCGAACAACG 1091123
Qy 73 ProArgProAaPProTTPProAlaGly----- 82
Db 1091122 CCGATGCG 1091066

Qy 83 -----ProGlnProProGluAaPProTTPProProAlaProGluValAaPleuArg 99
Db 1091065 CCGAGACCCCAAGTCCGCGGAGGACCACTGCGCGCGCGCGCGCGCGCGCGCGCG 1091015
Qy 100 ProGlnGluGluProAaPleuAaPPro 108
Db 1091014 CCGAATGACAGCCCG 1090988

RESULT 3
US-09-103-840A-1/c
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; FILE REFERENCE: 24366-2007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1

Alignment Scores:
Pred. No.: 0.143 Length: 4411529
Score: 198.50 Matches: 51
Percent Similarity: 32.54% Conservative: 4
Best Local Similarity: 30.18% Mismatches: 45
Query Match: 28.68% Indels: 69
DB: 3 Gaps: 6

US-09-994-365-3 (1-114) x US-09-103-840A-1 (1-4411529)

Qy 5 ProSerHisProProAlaGluAaPArgGluGluAaGlySerProThrLeuProGlnGly 24
Db 1091485 CCGCCGATGCGCGCGCGCGCGCGCGCTCCGCGCGCGCTCGCGCGCGCGCGCAACGCG 1091426
Qy 25 ProProValProGlyAaPProTTPProGlyAlaProProLeuPheGluAaPPro----- 42
Db 1091425 CCACTACCGCGCGCGCGCGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCTG 1091366
Qy 43 -----ProProThrArgProSerArg 49
Db 1091365 CCGCGCATCCCAACCGCGCGCAACCGATCCCGCGCGCGCGCGCGCGCGCGCGCGCG 1091306
Qy 50 ProTTP-----ArgAaPleuPro 55
Db 1091305 CCGTGGCGCGCTGCTCAACCATGCGCGATGCGCTCAAGCGCGCGCGCGCGCGCTGCG 1091246
Qy 56 GluThrGlyValTTPProProGluProProArgThraP----- 68
Db 1091245 CCAAGACCGCGCTGCG 1091186
Qy 69 -----ProProGlnPro 72
Db 1091185 CCGAACAACG 1091126
Qy 73 ProArgProAaPProTTPProAlaGly----- 82
Db 1091125 CCGATGCG 1091069
Qy 83 -----ProGlnProProGluAaPProTTPProProAlaProGluValAaPleuArg 99
Db 1091068 CCGAGACCCCAAGTCCGCGGAGGACCACTGCGCGCGCGCGCGCGCGCGCGCGCGCG 1091018


```
Qy      100 ProGlnGluGluProAspLeuAspPro 108
Db      1091017 CCGAATAGCAGACCCCGCGTTCCGCCG 1090991

RESULT 4
US-09-249-585A-4
; Sequence 4, Application US/09249585A
; Patent No. 6417002
; GENERAL INFORMATION:
; APPLICANT: HORLICK, Robert
; TITLE OF INVENTION: METHOD FOR MAINTENANCE AND SELECTION OF EPISOMES
; FILE REFERENCE: 0867/0D905
; CURRENT APPLICATION NUMBER: US/09/249,585A
; CURRENT FILING DATE: 1999-02-11
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 1926
; TYPE: DNA
; ORGANISM: Epstein Barr Virus
; NAME/KEY: misc_feature
; LOCATION: (1)..(1926)
; OTHER INFORMATION: template strand of EBNA-1 DNA
US-09-249-585A-4

Alignment Scores:
Pred. No.:      0.000192      Length:      1926
Score:          190.50        Matches:      47
Percent Similarity: 46.36%    Conservative: 4
Best Local Similarity: 42.73%  Mismatches:    48
Query Match:    27.53%       Indels:       11
DB:             4            Gaps:          4

US-09-994-365-3 (1-114) x US-09-249-585A-4 (1-1926)
Qy      5 ProSerHisProProAlaGluAspArgGluGluAlaGlySerProThrLeuProGlnGly 24
Db      553 CCGTCTCTCTCTCCCGCTCCCTCCCGCT-----CTCCCGCTCTCTCTCT 597
Qy      25 ProProValProGlyAspProTrpProGlyAlaProProLeuPheGluAspPro----- 42
Db      598 CCGTCCCGCTCGTCTCCCGCTCCCGCTCCCGCTCCCGCTCCCGCTCCCGCTCC 657
Qy      43 ---ProProThrArgProSerArgProTrpArgAspLeuProGluThrGlyValTrpPro 61
Db      658 CGTCTCTCTCTCCCGCTCCCGCTCCCGCTCCCGCTCCCGCTCCCGCTCCCGCTCC 717
Qy      62 ---ProGluProProArgThrAspProGlnProProArgProAspAspProTrpPro 80
Db      718 CGTCTCTCTCTCCCGCTCCCGCTCCCGCTCCCGCTCCCGCTCCCGCTCCCGCTCC 777
Qy      81 AlaGlyProGlnProProGluAsnProTrpProProAlaProGluValAspAsnArgPro 100
Db      778 CCCGCTCTCTCTCCCGCTCCCGCTCCCGCTCCCGCTCTCTCTCTCCCGCTCCCGCT 837
Qy      101 GlnGluGluProAspLeuAspProProArg 110
Db      838 CGTCTCTCTCTCC-----CGTCTCTCTCTCT 861

RESULT 5
US-09-130-114-2
; Sequence 2, Application US/09130114
; Patent No. 5976807
; GENERAL INFORMATION:
; APPLICANT: HORLICK, Robert A.
; APPLICANT: DAMAJ, Bassem B.
; APPLICANT: ROBBINS, Alan K.
; TITLE OF INVENTION: Eukaryotic Cells Stably Expressing Genes
; FILE REFERENCE: 0867/ID903US1
; CURRENT APPLICATION NUMBER: US/09/130,114
```

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; CURRENT FILING DATE: 1998-08-06
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 1931
; TYPE: DNA
; ORGANISM: EBNA
US-09-130-114-2

Alignment Scores:
Pred. No.:      0.000192      Length:      1931
Score:          190.50        Matches:      47
Percent Similarity: 46.36%    Conservative: 4
Best Local Similarity: 42.73%  Mismatches:    48
Query Match:    27.53%       Indels:       11
DB:             2            Gaps:          4

US-09-994-365-3 (1-114) x US-09-130-114-2 (1-1931)
Qy      5 ProSerHisProProAlaGluAspArgGluGluAlaGlySerProThrLeuProGlnGly 24
Db      553 CCGTCTCTCTCTCCCGCTCCCTCCCGCT-----CTCCCGCTCTCTCTCT 597
Qy      25 ProProValProGlyAspProTrpProGlyAlaProProLeuPheGluAspPro----- 42
Db      598 CCGTCCCGCTCGTCTCCCGCTCCCGCTCCCGCTCCCGCTCCCGCTCCCGCTCC 657
Qy      43 ---ProProThrArgProSerArgProTrpArgAspLeuProGluThrGlyValTrpPro 61
Db      658 CGTCTCTCTCTCCCGCTCCCGCTCCCGCTCCCGCTCCCGCTCCCGCTCCCGCTCC 717
Qy      62 ---ProGluProProArgThrAspProGlnProProArgProAspAspProTrpPro 80
Db      718 CGTCTCTCTCTCCCGCTCCCGCTCCCGCTCCCGCTCCCGCTCCCGCTCCCGCTCC 777
Qy      81 AlaGlyProGlnProProGluAsnProTrpProProAlaProGluValAspAsnArgPro 100
Db      778 CCCGCTCTCTCTCCCGCTCCCGCTCCCGCTCCCGCTCTCTCTCTCCCGCTCCCGCT 837
Qy      101 GlnGluGluProAspLeuAspProProArg 110
Db      838 CGTCTCTCTCTCC-----CGTCTCTCTCTCT 861

RESULT 6
US-09-103-840A-2
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

Alignment Scores:
Pred. No.:      0.654        Length:      4403765
Score:          188.50        Matches:      54
Percent Similarity: 40.67%    Conservative: 7
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```

Best Local Similarity: 36.00%      Mismatches: 32
Query Match:          27.24%      Indels:    57
DB:                   3           Gaps:     10

US-09-994-365-3 (1-114) x US-09-103-840A-2 (1-4403765)

QY      5 ProSerHisPProPfoAlaGluAspArgGluGluAla-----GlySerProThr 20
Db       2797465 CCGCCGCAGACCCACCAAGCCCCGGCTCAGGCTCCGCCGCCGCCGTACCAACCGTGCCTG 2797524
QY      21 ---LeuProGlnGlyProProValProGlyAspProTrpProGlyAlaProProLeuPhe 39
Db       2797525 TGAATTCCCGCGGCGCCACCGGCCCG-----CCGTGCTTCGCCGCCACCGCTG-- 2797575
QY      40 GluAspProProProThnArgProSerSerArgProTrpParGAspLeuProGluThnGly--- 58
Db       2797576 -----CCGCGTGCAAGCCGTCAAGCCCTTTAGATG-----GAGTCCGGGGAGC 2797620
QY      59 -----ValTrpProProGluPro----- 64
Db       2797621 CAACCCGCGCACCGCGCGCCGCGCTTCCTCCCTCCGCGCGGTCGCGCGCGTC 2797680
QY      65 -----ProArgHtnAspProProGln----- 71
Db       2797681 ATCCCGCGTCGCGCGCCGCCGCCCGCTGTCTACCAACCCGCGCGCGCGGCGCTG 2797740
QY      72 ProProArgPProAspAspProTrpPro----- 80
Db       2797741 CCGCGCCGCGCGACGCCCACTTTGGCGCGCGGTCCGCGCGTCCGCGCGTCCGAGAAT 2797800
QY      81 AlaGlyProGlnProProGluAsnProTrpProProAlaProGluValAspAsnArgPro 100
Db       2797801 GCTCGCCGCGCGCCACCGCCACCGCGCGCCACCGCCA-----CCG 2797845
QY      101 GlnGluGlnProAspLeuAspProProArg 110
Db       2797846 TTGCCCGCACGACGCTGAGCCCTTCGAGG 2797875

RESULT 7
US-09-103-840A-1
; Sequence 1, Application US/09103840A
; Patent No. 6294328
GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
FILE REFERENCE: 24366-20007 00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 1
LENGTH: 4411529
TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
OTHER INFORMATION: H37Rv
US-09-103-840A-1

Alignment Scores:
Pred. No.:      0.655      Length:      4411529
Score:         188.50      Matches:     54
Percent Similarity: 40.67%      Conservative: 7
Best Local Similarity: 36.00%      Mismatch:   32
Query Match:    27.24%      Indels:     57
DB:             3           Gaps:       10

US-09-994-365-3 (1-114) x US-09-103-840A-1 (1-4411529)
QY      5 ProSerHisPProPfoAlaGluAspArgGluGluAa-----GlySerProthr 20

```

```
Db      2802012 CCGCCGACGCCACCAGCCCCGGCTTAAGGCCTTCGGSCCCC GCCGTCAACCA CGTGC GCGATC 2802071
Qy      21 ---LeuProGlnGlyProProValProGluAspProTrtPProGlyAlaProProLeuPhe   39
           ::::| ||||| |
Db      2802072 TGAATTCCGCGCGGCCA CCGCCG-----CGTGCGCTCCCGCCCA CGCGCT-- 2802122
Qy      40 GlusApProProTrnHArgProSerArgProTraPratgAspleuProGluThrGly--- 58
           ||||||| ::::::| ::::| :|||:|
Db      2802123 -----CGCGCTGCAACCCCTTCAGCCCTTTAGTG-----GAGTCCGGCGAC 2802167
Qy      59 -----ValTrpProGluPro----- 64
           ::::| ||||| |
Db      2802168 CAACCGCGCACCGCGCGCGCGCTGTGCTCCCTGGCGCGCGGTTCGCGCGCGCTTC 2802227
Qy      65 -----ProArthrAspProGln---- 71
           ::::| ||||| |
Db      2802228 ATCCCGCGTCGCCGCCGCCGCCGCCGCGTCCAACAACCCGCCGCGCGCGSGGCGTG 2802288
Qy      72 ProProArgProAspAspProTrtPro----- 80
           CCGCGCGCGCGCGCCACTTTGGCGCGCGCGCTCCGCCGTCCCGCGCTGCCAGAATA 2802347
Db      Db      81 AlaGlyProGlnProProGluAsnProTrtProProAlaProGluValAspAsmArgPro 100
           ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy      Qy      2802348 GCTCCGCGCGGCCAACGACCCCA CGCGCGCACCA GCCCA-----CCG 2802397
           ::::| ||||| |
Db      2802393 TTGCCGCGACGACGCTGAGCCCTCCGAGG 2802422
RESULT 8
US-10-148-806-3
; Sequence 3, Application US/10148806
; Patent No. 6762042
; GENERAL INFORMATION:
; APPLICANT: Metzger, Michael
; APPLICANT: Liu, Xiaomei
; TITLE OF INVENTION: DNA MOLECULES ENCODING HUMAN NHL, A DNA
; FILE REFERENCE: 20585P
; CURRENT FILING DATE: 2002-06-05
; PRIOR APPLICATION NUMBER: US00/33065
; PRIOR FILING DATE: 2000-12-09
; PRIOR APPLICATION NUMBER: 60/169,970
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FaalSeq for windows Version 4.0
; SEQ ID NO 3
; LENGTH: 114793
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-148-806-3

Alignment Scores:
Pred. No.:          0.0437         Length:        114793
Score:             182.00         Matches:         42
Percent Similarity:    39.25%     Conservative:    0
Best Local Similarity: 39.25%     Mismatches:       55
Query Match:         26.30%     Indels:          10
DB:                  4            Gaps:              1

US-09-994-365-3 (1-114) x US-10-148-806-3 (1-114793)
Qy      3 GlyHisProSeHisBProProAlaGluAsparGluGluAlaGlySerProThrlreupro 22
           GGAGCTTCACCTTCCACCAAGACAGCAGCAGCAACCTTCACCATCACCACCACT 82588
Db      82529 GGGAGCTTCACCTTCCACCAAGACAGCAGCAGCAACCTTCACCATCACCACCACT 82588
Qy      23 GInglyProProValProGlyAspProTrtPProGlyAlaProProleuPhelGluaspro 42
           ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      82589 CCACGACGACGACCTTCACCACTTCACCACTTCACCACTTCACCACTTCACCACTTCACCA 82648
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QY 43 ProProtharProSerarProTprArgAspleuProglunhlyValtrProPro 62
 Db 82649 CCACCACACCACTCCACCA-----CCACCA 82678
 QY 63 GluProProArghtrArpProProgluProProArghtrArpProProglu 82
 Db 82679 CCACCACCTCCACCAACCAACCAACCAACCAACCACTCCACCACTCCACCA 82738
 QY 83 ProgluProgluAsnProTprProgluProgluValAspAsnArpProglu 102
 Db 82739 CCTCACCTCCACCAACCAACCAACCACTCCACCACTCCACCACTCCACCA 82798
 QY 103 GluProAspleuAspProPro 109
 Db 82799 CCACCACCTCCACCAACCA 82819
 RESULT 9
 US-08-146-930-1/c
 Sequence 1, Application US/08146930
 Patent No. 5958764
 GENERAL INFORMATION:
 APPLICANT: Roop, Dennis R.
 APPLICANT: Rothmangel, Joseph A.
 TITLE OF INVENTION: SPECIFIC EXPRESSION VECTORS
 TITLE OF INVENTION: AND METHODS OF USE
 NUMBER OF SEQUENCES: 4
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: LYON & LYON
 STREET: 611 West Sixth Street
 CITY: Los Angeles
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 90017
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: IBM MS-DOS (Version 5.0)
 SOFTWARE: WordPerfect (Version 5.1)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/146,930
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 PRIOR APPLICATION DATA: including application
 PRIOR APPLICATION DATA: described below: two
 APPLICATION NUMBER: 07/876,286
 FILING DATE: April 30, 1992
 APPLICATION NUMBER: No. 5958764 yet assigned (204/132)
 FILING DATE: October 29, 1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Warburg, Richard J.
 REGISTRATION NUMBER: 32,327
 REFERENCE/DOCKET NUMBER: 204/152
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440
 TELEX: 67-3510
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 6530 bases
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 US-08-146-930-1
 Alignment Scores:
 Pred. No.: 0.0028 Length: 6530
 Score: 181.00 Matches: 50
 Percent Similarity: 39.60% Conservative: 9
 Best Local Similarity: 33.56% Mismatches: 46
 Query Match: 26.16% Indels: 44

DB: 2 Gaps: 6
 US-09-994-365-3 (1-114) x US-08-146-930-1 (1-6530)
 QY 8 ProProAlaGluAspArgGluGluAlaGlySerProThrIleu-----21
 Db 4081 CCACCTCCAGAGCGCCGACCAAGAGAGCGCGCTCCGAGAGCAACCGCTCCGCT 4022
 QY 22 -----ProgluGlyProProVal-----ProgluAspProTprProglu 35
 Db 4021 CCGAGTAGCCTCTCCGAGCAACCGCGCTGCTCCGAGAGCAACCTCCGAGCA 3962
 QY 36 ProProleu---PheGluAspProProProThrArpProSerArpProTprArgAspleu 54
 Db 3961 CCGCGCTGCCCCCGGAGAGCGCGCCGCAAGCCACCGCGCTCCGAGTAGCCTCC 3902
 QY 55 ProgluThrGlyValTprProProgluProProArghtrArpProgluProProArg 74
 Db 3901 CCGCAGCCACCGCTGCGCGCCGACCAACCGCTGAGTAGCAGCCAGCGCGCCGCG 3842
 QY 75 ProAspAspProTprProAlaGlyProgluProProgluAsnPro-----89
 Db 3841 CCAGAGAGCCACCTCCACAGCTACCTCTCCGAGAGAGCCCTCCGAGTAGCTTC 3782
 QY 90 TTP-----ProProAlaProglu 95
 Db 3781 TGGGGGGCGCAGAGGCTGCTGCTGCTGAGAGAGTAGTATAGCCCTCCGCGCGCA 3722
 QY 96 ValAspAsnArpProglu-----GluGlu 103
 Db 3721 GAGAGCGCGCGCGCGAGCTGCCACCGCACCGGATAGCGCGCGCGCTGCG 3662
 QY 104 ProAspleuAspProProArghtrGlu 112
 Db 3661 CCGCACTGAGCCACCAACCAAGAG 3635
 RESULT 10
 US-08-458-240-1/c
 Sequence 1, Application US/08458240
 Patent No. 6143727
 GENERAL INFORMATION:
 APPLICANT: Roop, Dennis R.
 APPLICANT: Rothmangel, Joseph A.
 TITLE OF INVENTION: SPECIFIC EXPRESSION VECTORS
 TITLE OF INVENTION: AND METHODS OF USE
 NUMBER OF SEQUENCES: 4
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: LYON & LYON
 STREET: 611 West Sixth Street
 CITY: Los Angeles
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 90017
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: IBM MS-DOS (Version 5.0)
 SOFTWARE: WordPerfect (Version 5.1)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/458,240
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/146,930
 FILING DATE:
 APPLICATION NUMBER: 07/876,286
 FILING DATE: April 30, 1992
 APPLICATION NUMBER: No. 6143727 yet assigned (204/132)
 FILING DATE: October 29, 1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Warburg, Richard J.
 REGISTRATION NUMBER: 32,327

REFERENCE/DOCKET NUMBER: 204/152
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 488-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 6530 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-458-240-1

Alignment Scores:
Pred. No.: 0.0028 Length: 6530
Score: 181.00 Matches: 50
Percent Similarity: 39.60% Conservative: 9
Best Local Similarity: 33.56% Mismatches: 46
Query Match: 26.16% Indels: 44
DB: 3 Gaps: 6

US-09-994-365-3 (1-114) x US-08-458-240-1 (1-6530)

QY 8 ProProAlaGluAspArgGluGluAlaGlySerProThrLeu----- 21
DB 4081 CCACTCCAGAGCCGCCACAGAGAGCCGCTCCGAGCTGAGAGCCACCGCTCCGCT 4022

QY 22 -----ProGInGlyProProVal---ProGlyAspProTTPProGlyAla 35
DB 4021 CCGAGTAGCTCTCCGACAGCCAGCCGCTCCGAGTAGAGAGCCACTCCGAGCCA 3962

QY 36 ProProLeu---PheGluAspProProThrArgProSerArgProTTPArgAspLeu 54
DB 361 CCGCGCTGCCCCCGGAGAGCCGCGCCAGAGCCACCGCCCTCCGAGTAGCTCCA 3902

QY 55 ProGluThrGlyValTTPProProGluProProArgThraAspProProGluProProArg 74
DB 3901 CCGAGAGCCAGCTCTCCGACAGCCAGCCGCTGAGTAGAGAGCCACCGCCGCG 3842

QY 75 ProAspAspProTTPProAlaGlyProGluProProGluAspPro----- 89
DB 3841 CCAAGAGAGCCACTCCACAGCTACCTCTCCGAGAGAGCCCTCCGAGTAGCTGCG 3782

QY 90 TTP-----ProProAlaProGlu 95
DB 3781 TGGGGGGCGGAGAGCTGTACTGCTGTGAGAGAGTATAGCCCCCTCCGCGCCA 3722

QY 96 ValAspAsnArgProGln-----GluGlu 103
DB 3721 GAGAGAGCCGCGCGGAGCTGTGACACCGCCAGATAGCCGCGCGCGCTGCG 3662

QY 104 ProAspLeuAspProProArgGluGlu 112
DB 3661 CCGCAACTGAGAGCCACCAAGAGAG 3635

RESULT 11
PCT-US93-03993-1/c
Sequence 1, Application PC/TUS9303993
GENERAL INFORMATION:
APPLICANT: Roop, Dennis R.
APPLICANT: Rothnagel, Joseph A.
APPLICANT: Greenhalgh, David A.
TITLE OF INVENTION: CONSTITUTIVE AND INDUCIBLE EPIDERMAL
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESS: Fulbright & Jaworski
STREET: 1301 McKinney, Suite 5100
CITY: Houston
STATE: Texas
COUNTRY: U.S.A.
ZIP: 77010-3095

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/03993
FILING DATE: 19930428
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Paul, Thomas D.
REGISTRATION NUMBER: 32,714
REFERENCE/DOCKET NUMBER: D-5405
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713/651-5325
TELEFAX: 713/651-5246
TELEX: 762829
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 6530 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
PCT-US93-03993-1

Alignment Scores:
Pred. No.: 0.0028 Length: 6530
Score: 181.00 Matches: 50
Percent Similarity: 39.60% Conservative: 9
Best Local Similarity: 33.56% Mismatches: 46
Query Match: 26.16% Indels: 44
DB: 5 Gaps: 6

US-09-994-365-3 (1-114) x PCT-US93-03993-1 (1-6530)

QY 8 ProProAlaGluAspArgGluGluAlaGlySerProThrLeu----- 21
DB 4081 CCACTCCAGAGCCGCCACAGAGAGCCGCTCCGAGCTGAGAGCCACCGCTCCGCT 4022

QY 22 -----ProGInGlyProProVal---ProGlyAspProTTPProGlyAla 35
DB 4021 CCGAGTAGCTCTCCGACAGCCAGCCGCTCCGAGTAGAGAGCCACTCCGAGCCA 3962

QY 36 ProProLeu---PheGluAspProProThrArgProSerArgProTTPArgAspLeu 54
DB 361 CCGCGCTGCCCCCGGAGAGCCGCGCCAGAGCCACCGCCCTCCGAGTAGCTCCA 3902

QY 55 ProGluThrGlyValTTPProProGluProProArgThraAspProProGluProProArg 74
DB 3901 CCGAGAGCCAGCTCTCCGACAGCCAGCCGCTGAGTAGAGAGCCACCGCCGCG 3842

QY 75 ProAspAspProTTPProAlaGlyProGluProProGluAspPro----- 89
DB 3841 CCAAGAGAGCCACTCCACAGCTACCTCTCCGAGAGAGCCCTCCGAGTAGCTGCG 3782

QY 90 TTP-----ProProAlaProGlu 95
DB 3781 TGGGGGGCGGAGAGCTGTACTGCTGTGAGAGAGTATAGCCCCCTCCGCGCCA 3722

QY 96 ValAspAsnArgProGln-----GluGlu 103
DB 3721 GAGAGAGCCGCGCGGAGCTGTGACACCGCCAGATAGCCGCGCGCGCTGCG 3662

QY 104 ProAspLeuAspProProArgGluGlu 112
DB 3661 CCGCAACTGAGAGCCACCAAGAGAG 3635

RESULT 12
US-09-894-844-103/c
Sequence 103, Application US/09894844

LENGTH: 1280
TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
US-09-670-314-4

Alignment Scores:

Pred. No.:	Score:	Length:	Matches:	Conservative:
	180.00		49	
Percent Similarity:	44.00%		6	
Best Local Similarity:	39.20%	Mismatches:	53	
Query Match:	26.01%	Indels:	17	
DB:	4	Gaps:	6	

US-09-994-365-3 (1-114) x US-09-670-314-4 (1-1280)

```
Qy 5 ProserHisProProAlaGluAspArgGluGluGlySerProThrLeuProGlnGly 24
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 869 CCACCGGCGCCCGCGGTGTCGCCGACGCTTAAGGCTGCGCCGCTTCGACGCGGCGCG 810
Qy 25 -----ProProValProGlyAspProTrpProGlyAlaProProLeu 38
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 809 CCGGTAACCCCACTAGCTAGCCCGCGGTGCC-----CGTTCCACGCGCGCGCGCTTA 756
Qy 39 PheGluAspPro---ProProThrArgProSerArgProTrpArgAspLeuProGluThr 57
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 755 GCGTTACCGCGCATTCGCGCGATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCATTG 696
Qy 58 GlyValTrpProProGluProProArgThr---AspProProGlnProProArgPro--- 75
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Db 695 CCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 636
Qy 76 -----AspAspProTrp-----ProAlaGlyProGlnProProGluAsnProTrp 90
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 635 CTGACAACAGCAGCGCGCGCGCTTGCCACCGCGCGCGCGCGCGCGCGCGCGCGCGCAAT 576
Qy 91 ProProAlaProGluValAspAsnArgProGlnGluGluProAspLeuAspPro-ProAr 110
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Db 575 CCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 516
Qy 110 gglugluTrpArg 114
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Db 515 CCGTCCCGCACCGG 503
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RESULT 15

US-09-128-155-16
Sequence 16, Application US/09128155
Patent No. 6117654
GENERAL INFORMATION:
APPLICANT: Pan, Yang
TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
FILE REFERENCE: 09404/052001
CURRENT APPLICATION NUMBER: US/09/128,155
CURRENT FILING DATE: 1998-08-03
EARLIER APPLICATION NUMBER: US 60/091,650
EARLIER FILING DATE: 1998-07-02
EARLIER APPLICATION NUMBER: US 60/054,646
EARLIER FILING DATE: 1997-08-04
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 16
LENGTH: 152331
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(152331)
OTHER INFORMATION: n = A,T,C or G
US-09-128-155-16

Alignment Scores:

Pred. No.:	Score:	Length:	Matches:
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Percent Similarity:	40.00%	Conservative:	1
Best Local Similarity:	39.13%	Mismatches:	56
Query Match:	25.94%	Indels:	14
DB:	3	Gaps:	2

US-09-994-365-3 (1-114) x US-09-128-155-16 (1-152331)

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Qy 8 ProProAlaGluAspArgGluGluAlaGlySerProThrLeuProGlnGlyProProVal 27
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Db 21934 CCCCCCCCCCCCCCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 21993
Qy 28 ProGly---AspProTrpProGlyAlaProProLeuPheGluAspProProProThrArg 46
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Qy 47 ProSerArgProTrpArgAspLeuProGluThrGlyValTrpProProGluProProArg 66
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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Qy 67 Thr-----AspProProGlnProProArg 74
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Db 22114 AGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 22173
Qy 75 ProAspAspProTrpProAlaGlyProGlnProProGluAsnProTrpProProAlaPro 94
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Db 22174 CCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 22231
Qy 95 GluValAspAsnArgProGlnGluGluProAspLeuAspProPro 109
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Search completed: January 12, 2005, 21:17:28
Job time : 6198 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus.p2n model

Run on: January 12, 2005, 16:40:28 ; Search time 454 Seconds

(without alignments)
1442.800 Million cell updates/sec

Title: US-09-994-365-3

Perfect score: 692

Sequence: 1 SEGHPSPHAPDEAREAGSPR.....EVDNRQEPEDLPDPREYR 114

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Ygapop 10.0 , Ygapext 0.5	
Fgapop 6.0 , Fgapext 7.0	
Delop 6.0 , Delext 7.0	

Searched: 4300275 seqs, 2872944193 residues

Total number of hits satisfying chosen parameters: 8600550

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-TRANS=human40.csl -LIST=45 -DOCCALIGN=200 -THR SCORE=0 -WAIT -DSBLOCCK=100
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-MAXLEN=2000000000 -USER=US0994365 @CGN_1_1_480@runat_12012005_164014_11190
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-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
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Database: Published Applications_NA:*

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3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
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18: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
19: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	692	100.0	891	9	US-09-994-365-1	Sequence 1, Appl
2	692	100.0	2997	9	US-09-994-365-10	Sequence 10, Appl
3	692	100.0	3001	9	US-09-994-365-4	Sequence 4, Appl
4	692	100.0	25235	15	US-10-164-230-2	Sequence 2, Appl
5	692	100.0	55050	17	US-10-467-752-4	Sequence 4, Appl
6	486	70.2	565	15	US-10-029-386-5700	Sequence 5700, Ap
7	441	63.7	367378	15	US-10-312-841-1	Sequence 1, Appl
8	314	45.4	157	15	US-10-029-386-19510	Sequence 19510, A
9	199	28.8	711	16	US-10-282-122A-31860	Sequence 31860, A
10	198.5	28.7	2772	16	US-10-282-122A-28290	Sequence 28290, A
11	197	28.3	573	17	US-10-767-701-4301	Sequence 4301, Ap
12	196	28.5	766	18	US-10-425-115-82176	Sequence 82176, A
13	193	27.9	985	18	US-10-425-115-91623	Sequence 91623, A
14	190.5	27.5	446	9	US-09-864-761-20699	Sequence 20699, A
15	190	27.5	420	17	US-10-021-332-5998	Sequence 5998, Ap
16	189.5	27.4	815	16	US-10-424-599-20495	Sequence 20495, A
17	188.5	27.2	600	18	US-10-363-345A-39087	Sequence 39087, A
18	188.5	27.2	600	18	US-10-363-345A-39088	Sequence 39088, A
19	188	27.2	545	17	US-10-437-963-56258	Sequence 56258, A
20	188	27.2	1493	15	US-10-029-386-25133	Sequence 25133, A
21	187.5	27.1	916	18	US-10-425-115-47293	Sequence 47293, A
22	187.5	27.1	1327	16	US-10-398-221-1365	Sequence 1265, Ap
23	186.5	27.0	629	17	US-10-021-323-9375	Sequence 9375, Ap
24	186	26.9	925	17	US-10-437-963-44536	Sequence 44536, A
25	186	26.9	1455	16	US-10-282-122A-28683	Sequence 28683, A
26	186	26.9	12733	14	US-10-032-393-47	Sequence 47, Appl
27	186	26.9	12739	14	US-10-032-393-8	Sequence 8, Appl
28	185.5	26.8	588	17	US-10-021-323-9377	Sequence 9377, Ap
29	185.5	26.8	1245	17	US-10-437-963-94850	Sequence 94850, A
30	185.5	26.8	1744	17	US-10-437-963-19774	Sequence 19774, A
31	184.5	26.8	485	16	US-10-424-599-65670	Sequence 65670, A
32	183.5	26.5	3163	15	US-10-017-161-1857	Sequence 1857, Ap
33	183.5	26.5	3163	15	US-10-292-795-1513	Sequence 1513, Ap
34	183	26.4	590	18	US-10-425-115-133228	Sequence 133228, A
35	182.5	26.4	1083	15	US-10-029-386-20723	Sequence 20723, A
36	182	26.3	717	16	US-10-424-599-121376	Sequence 121376, A
37	182	26.3	821	18	US-10-425-115-11043	Sequence 11043, A
38	182	26.3	1888	16	US-10-282-122A-28602	Sequence 28602, A
39	182	26.3	114739	15	US-10-148-806-3	Sequence 3, Appl
40	181.5	26.2	903	17	US-10-437-963-85740	Sequence 85740, A
41	181	26.2	674	16	US-10-424-599-69089	Sequence 69089, A
42	181	26.2	778	16	US-10-424-599-54839	Sequence 54839, A
43	181	26.2	791	16	US-10-424-599-64474	Sequence 64474, A
44	181	26.2	862	17	US-10-437-963-28390	Sequence 28390, A
45	180.5	26.1	497	16	US-10-424-599-133788	Sequence 133788, A

ALIGNMENTS

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RESULT 1
US-09-994-365-1
; Sequence 1, Application US/0994365
; Patent No. US20020115148A1
; GENERAL INFORMATION:
; APPLICANT: Charmsley, Patrick
; APPLICANT: Moss, Patrick
; TITLE OF INVENTION: Compositions and Methods for Diagnosing or Treating Psoriasis
; FILE REFERENCE: CECH18109
; CURRENT APPLICATION NUMBER: US/09/994,365
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: US 60/253,592
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 60/256,839
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 891
; TYPE: DNA

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Db 2397 CCCCCGAGCCGCTAGACGATCTCTCAACCTCCCGCCTGACGACCTTGCCG 2456
 Qy 81 AlaglyProgluProProgluAenProProgluProgluAaPpaAaPro 100
 Db 2457 GCGAGAGCCCAAGCCCAAGAAACCCCTGCTCTGCTGAGGAGGACCACT 2516
 Qy 101 GlnGluGluProAaPleuAaPleuProProAaGluGluArg 114
 Db 2517 CAGAGAGGAGCCAGACCTAGACCCACCCCGGAGAGATACAGA 2558

RESULT 4

US-10-164-230-2
 ; Sequence 2, Application US/10164230
 ; Publication No. US20030170652A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Inoko, Hidetoshi
 ; APPLICANT: Tamiya, Gen
 ; TITLE OF INVENTION: METHOD OF TESTING FOR PSORIASIS VULGARIS
 ; FILE REFERENCE: 06501-112US1
 ; CURRENT APPLICATION NUMBER: US/10/164,230
 ; CURRENT FILING DATE: 2002-09-04
 ; PRIOR APPLICATION NUMBER: PCT/JP00/08624
 ; PRIOR FILING DATE: 2000-12-06
 ; PRIOR APPLICATION NUMBER: JP 11/346867
 ; PRIOR FILING DATE: 1999-12-06
 ; NUMBER OF SEQ ID NOS: 63
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 2
 ; LENGTH: 25235

;; TYPE: DNA
 ;; ORGANISM: Homo sapiens
 ;; FEATURE:
 ;; NAME/KEY: exon
 ;; LOCATION: (1)...(420)
 ;; FEATURE:
 ;; NAME/KEY: exon
 ;; LOCATION: (1282)...(1405)
 ;; FEATURE:
 ;; NAME/KEY: exon
 ;; LOCATION: (1602)...(1702)
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 ;; LOCATION: (2352)...(2364)
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 ;; LOCATION: (6287)...(6509)
 ;; FEATURE:
 ;; NAME/KEY: exon
 ;; LOCATION: (10417)...(10493)
 ;; FEATURE:
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 ;; LOCATION: (14244)...(14407)
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 US-10-164-230-2

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 Query Match: 100.00% Indels: 0
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US-09-994-365-3 (1-114) x US-10-164-230-2 (1-25235)

Qy 1 SerGluGluYhiAsProSerHiAsProProAlaGluAsPArgGluGluAgiYSerProThr 20
 Db 1766 AGCAGAGGAGCCACCTCTCTCAACCCGACGAGACGAGAGGAGGCTCCCAACA 1825
 Qy 21 LeuProGluGluProProValAProGluAaPProProGluAaProPheGlu 40
 Db 1826 TTGCTTAGGGAGCCCAAGTCCCGGTGACCTTGGCAGAGGAGCCCTCTCTTGA 1885
 Qy 41 AspProProProThrArgProSerArgProTrpArgAsPleuProGluThrGluValTrp 60
 Db 1886 GATCTCCGCTTACCCGCCCACTGCTGCTGAGAGACCTGCTGAACTGAGGTGG 1945
 Qy 61 ProProGluProProArgThrAsPProProGluProProArgProAaPProTrpPro 80
 Db 1946 CCCCCTAACCCTAGACGATCTCTCAACTCCCGGCTGACGACCTTGCCG 2005
 Qy 81 AlaglyProgluProProgluAenProProgluProgluAaPpaAaPro 100
 Db 2006 GCGAGAGCCCAAGCCCAAGAAACCCCTGCTCTGCTGAGGTGACCAACGACT 2065
 Qy 101 GlnGluGluProAaPleuAaPleuProProAaGluGluArg 114
 Db 2066 CAGAGAGGAGCCAGACCTAGACCCACCCGGAGAGATACAGA 2107

RESULT 5

US-10-467-752-4
 ; Sequence 4, Application US/10467752
 ; Publication No. US20040161759A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Lench, et al.
 ; TITLE OF INVENTION: Test and Model for Inflammatory disease
 ; FILE REFERENCE: 2003882-0009
 ; CURRENT APPLICATION NUMBER: US/10/467,752
 ; CURRENT FILING DATE: 2003-08-13
 ; PRIOR APPLICATION NUMBER: PCT/GB02/00653
 ; PRIOR FILING DATE: 2002-02-13
 ; PRIOR APPLICATION NUMBER: GB0103514.6
 ; PRIOR FILING DATE: 2001-02-13
 ; NUMBER OF SEQ ID NOS: 109
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 4
 ; LENGTH: 55050

;; TYPE: DNA
 ;; ORGANISM: Homo sapiens
 ;; FEATURE:
 ;; NAME/KEY: misc_feature
 ;; LOCATION: (13351)..(13351)
 ;; OTHER INFORMATION: n is a or t or g or c
 ;; FEATURE:
 ;; NAME/KEY: misc_feature
 ;; LOCATION: (13401)..(13401)
 ;; OTHER INFORMATION: n is a or t or g or c
 US-10-467-752-4

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Pred. No.: 3.32e-46 Length: 55050
 Score: 692.00 Matches: 114
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 Query Match: 100.00% Indels: 0
 DB: 17 Gaps: 0

US-09-994-365-3 (1-114) x US-10-467-752-4 (1-55050)

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 Qy 21 LeuProGluGluProProValAProGluAaPProProGluAaProPheGlu 40
 Db 27171 TTGCTTAGGGAGCCCAAGTCCCGGTGACCTTGGCAGAGGAGCCCTCTCTTGA 27230
 Qy 41 AspProProProThrArgProSerArgProTrpArgAsPleuProGluThrGluValTrp 60

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Qy 61 ProProGluProProArgThrAspProGlnProProAlaGlyProAlaAspProTyrPro 80
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Qy 81 AlaGlyProGlnProProGluAsnProTyrProProAlaProGluValAspAsnArgPro 100
Db 27351 GCAGAGACCCGAGCCCGAGAAACCCCTGCTCTGCTCCCTGAGTGGACACCACT 27410
Qy 101 GlnGluGluProAspLeuAspProProArgGluGluTyrArg 114
Db 27411 CAGAGAGACCGAGCCTAGACCCCGGAGAGAGTACAGA 27452

RESULT 6
US-10-029-386-5700
; Sequence 5700, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Hanzel, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
; FILE REFERENCE: AEOMICA-X-2
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 5700
; LENGTH: 565
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AB023060.1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.82
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.82
; OTHER INFORMATION: SWISSPROT HIT: Q99715, EVALU6 6.20e-01
; OTHER INFORMATION: EST HUMAN HIT: BF513178.1, EVALU6 0.00e+00
; OTHER INFORMATION: NT HIT: g115304354, EVALU6 0.00e+00
US-10-029-386-5700

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Qy 56 GlnThrGlyValTyrProProGluProProArgThrAspProGlnProProArgPro 75
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Db 121 GAGGACCTTGGCGGAGAGACCCGAGAAACCCCTGCTCTGCTCCGCTGAG 180
Qy 96 ValAspAsnArgProGlnGluGluProAspLeuAspProProArgGluGluTyrArg 114
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; Sequence 1, Application US/10312841
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; Publication No. US20030186277A1
; GENERAL INFORMATION:
; APPLICANT: Epigenomics AG
; TITLE OF INVENTION: Diagnose von bedeutenden genetischen Parametern innerhalb des WMC
; FILE REFERENCE: E01/1208/WO
; CURRENT APPLICATION NUMBER: US/10/312, 841
; CURRENT FILING DATE: 2002-12-30
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 1
; LENGTH: 3673778
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically created genomic DNA (Homo sapiens)
; NAME/KEY: unsure
; LOCATION: (3294164)
US-10-312-841-1

Alignment Scores:
Pred. No.: 1.36e-24 Length: 3673778
Score: 441.00 Matches: 69
Percent Similarity: 85.96% Conservative: 29
Best Local Similarity: 60.53% Mismatches: 16
Query Match: 63.73% Indels: 0
Gaps: 0

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Qy 21 LeuProGlnGluProProValProGluAspProTyrProGlyValAspProLeuPheGlu 40
Db 1425978 TTACCTTAACACCCCAATCCCGATACCTTAACCAAAACACCCCTCTTTTAA 1425919
Qy 41 AspProProProThrArgProSerArgProTyrParGAspLeuProGluThrGlyValTyr 60
Db 1425918 AATCTCCGCGCTACCGCCGCAATCGTCCCTAAACCAACTACTAAATAAATCTAA 1425859
Qy 61 ProProGluProProArgThrAspProProGlnProProArgProAspAspProTyrPro 80
Db 1425858 CCCCCTTAACCGGCTTAACGATCTCTCAACCTCCCGAGACTTAACGACCTTAACCG 1425799
Qy 81 AlaGlyProGlnProProGluAsnProTyrProProAlaProGluValAspAsnArgPro 100
Db 1425798 ACAAAACCCCAACCCCAACCAACCCCTTAACCTCTAACCCCTTAATAATTAACCA 1425739
Qy 101 GlnGluGluProAspLeuAspProProArgGluGluTyrArg 114
Db 1425738 CAAACCAACCAACCTTAACCAACCAACCAACCAACCAACCAACCAACCAACCA 1425697

RESULT 8
US-10-029-386-19510
; Sequence 19510, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Hanzel, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR GI
; FILE REFERENCE: AEOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029, 386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 19510
; LENGTH: 157
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
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OTHER INFORMATION: MAP TO AB023060.1
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.82
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.82
OTHER INFORMATION: EST_HUMAN_HIT: BF902421.1, EVALUATE 3.00e-03
OTHER INFORMATION: NT_HIT: g115304354, EVALUATE 2.00e-83
OTHER INFORMATION: SWISSPROT_HIT: P13889, EVALUATE 3.00e-01
US-10-029-386-19510

Alignment Scores:
Pred. No.: 1,34e-17 Length: 157
Score: 314.00 Matches: 51
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 45.38% Indels: 0
DB: 15 Gaps: 0

US-09-994-365-3 (1-114) x US-10-029-386-19510 (1-157)

QY 64 ProProArghThraPpProGlnProProArghProAspPpProTTPProAlaGlyPro 83
DB 2 CCGCTTGAACGATCTCTCTCAACCTCCCGCTCAACCTTGGCCGACGAGCCC 61
QY 84 GlnProGlnuAnProTTPProProAlaProGlnuAlaAspAnArgProGlnGlu 103
DB 62 CAGCCCCAGAAAACCCCTGGCTCTGCCCCCTGAGGTGAGCAACGACCTCAGGAGAG 121
QY 104 ProAspLeuAspProProAlaGlnGluTyrArg 114
DB 122 CAGACCTAGACCAACCCCGGAGAGTACAGA 154

RESULT 9

US-10-282-122A-31860/C

Sequence 31860, Application US/10282122A

Publication No. US20040029129A1

GENERAL INFORMATION:

APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Haselbeck, Cheryl
APPLICANT: Ohlsen, Karl
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.

APPLICANT: Xu, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

FILE REFERENCE: ELITRA.034A

CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT FILING DATE: 2003-02-20

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/230,335

PRIOR FILING DATE: 2000-09-06

PRIOR APPLICATION NUMBER: 60/230,347

PRIOR FILING DATE: 2000-09-09

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR FILING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: 60/267,636

PRIOR FILING DATE: 2001-02-09

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR FILING DATE: 2001-02-16

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OP SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 31860
LENGTH: 711
TYPE: DNA
ORGANISM: Pseudomonas putida
US-10-282-122A-31860

Alignment Scores:
Pred. No.: 7.86e-08 Length: 711
Score: 199.00 Matches: 46
Percent Similarity: 44.95% Conservative: 3
Best Local Similarity: 42.20% Mismatches: 42
Query Match: 28.76% Indels: 18
DB: 16 Gaps: 6

US-09-994-365-3 (1-114) x US-10-282-122A-31860 (1-711)

QY 5 ProSerHisProProAlaGluAspArgGluGluAlaGlySerProThrLeuProGlnGly 24
DB 446 CCGGATGCGCACCACCG-----TCACCGCGCTGCGG---TGG 411
QY 25 ProProValPro---GlyAspProTTPProGlyAlaProProLeuPheGluAspProPro 43
DB 410 CCACACTTCGCGCTTCGCGCACCATGCGCACCGCGCCGACACTT-----CCACACCA 357
QY 44 ProThrArgProSerArgProTTPArgAspLeuProGluThrGlyValTTPProGlu 63
DB 356 CCGGCGCACCATCACCGCGCTTCCACACCAACCG-----TGGCCACCGCCA 309
QY 64 ProProArghThraPp-----ProProGlnProProArghProAspPpProTTPPro 80
DB 308 CCGCGCTTCCACACCATCACCGTGACACCGCCGCGCTTCCACCGCACCGTGCGCA 249
QY 81 AlaGlyProGlnProProGluAnProTTPProProAlaProGlnuAlaAspAnArgPro 100
DB 248 CCGCGCGCGCGCTTCCACCGCGCGTGCGCACCGCGCGCGCATTCACCGCGCACCG 189
QY 101 GlnGluGluProAspLeuAspProPro 109
DB 188 TGGCCACCGCGCACCGCGCACCGCGCACCG 162

RESULT 10

US-10-282-122A-28290/C

Sequence 28290, Application US/10282122A

Publication No. US20040029129A1

GENERAL INFORMATION:

APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Haselbeck, Cheryl
APPLICANT: Ohlsen, Karl
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.

APPLICANT: Xu, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

FILE REFERENCE: ELITRA.034A

CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT FILING DATE: 2003-02-20

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/230,335

PRIOR FILING DATE: 2000-09-06

PRIOR APPLICATION NUMBER: 60/230,347

PRIOR FILING DATE: 2000-09-09

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RESULT 11
US-10-767-701-4301
; Sequence 4301, Application US/1076770D1
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei

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/ TYPE: DNA
/ ORGANISM: Zea mays
/ FEATURE:
/ OTHER INFORMATION: Clone ID: MRT4577_17495C.1
US-10-425-115-82176

Alignment Scores:
Pred. No.: 1,45e-07 Length: 766
Score: 196.00 Matches: 44
Percent Similarity: 41.51% Conservative: 0
Best Local Similarity: 41.51% Mismatches: 54
Query Match: 28.32% Indels: 8
DB: 18 Gaps: 2

US-09-994-365-3 (1-114) x US-10-425-115-82176 (1-766)
Qy 4 HisProSerHisProCProAlaGluAspArgGluAlaGlySerProThrLeuProGln 23
Db 165 CACCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCTCTCACCACCCCCCCCCC 224
Qy 24 GlyProProValProGlyAspProTrpProGlyAlaProProLeuPheGluAspPro 43
Db 225 CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC 284
Qy 44 ProThrArgProSerArgProTrpArgAspLeuProGluThrGlyAlaTrpProProGln 63
Db 285 CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC-----CCCCCCCC 329
Qy 64 ProProArgGThrAspProProGlnProProArgProAspAspProTrpProAlaGlyPro 83
Db 330 CCCCCCCCCCTCCCCCCCCCCCCCCCCCACCCCCCTCCACCCCCCCCCCCCCCCC 389
Qy 84 GlnProProGluAsnProTrpProProAlaProGluValAspAsnArgProGlnGln 103
Db 390 CCCCCCCCCCCCCCCCCCCCCCACCCCCCCCC-----GACCCACACCCCCAC 440
Qy 104 ProAspLeuAspProPro 109
Db 441 CCCCCCTCCCCCCCCC 458

RESULT 13
US-10-425-115-91623/C
/ Sequence 91623, Application US/10425115
/ Publication No. US20040214272A1
/ GENERAL INFORMATION:
/ APPLICANT: La Rosa, Thomas J.
/ APPLICANT: Kovalic, David K.
/ APPLICANT: Zhou, Yihua
/ APPLICANT: Cao, Yongwei
/ TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
/ TITLE OF INVENTION: Plants
/ FILE REFERENCE: 38-21(5322)B
/ CURRENT APPLICATION NUMBER: US/10/425,115
/ CURRENT FILING DATE: 2003-04-28
/ NUMBER OF SEQ ID NOS: 369326
/ SEQ ID NO 91623
/ LENGTH: 985
/ TYPE: DNA
/ ORGANISM: Zea mays
/ FEATURE:
/ NAME/KEY: unsure
/ LOCATION: (1)..(985)
/ OTHER INFORMATION: unsure at all n locations
/ FEATURE:
/ OTHER INFORMATION: Clone ID: MRT4577_183557C.1
US-10-425-115-91623

Alignment Scores:
Pred. No.: 3.06e-07 Length: 985
Score: 193.00 Matches: 45
Percent Similarity: 42.99% Conservative: 1
Best Local Similarity: 42.06% Mismatches: 51
Query Match: 27.89% Indels: 10

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DB: 18      Gaps: 3
US-09-994-365-3 (1-114) x US-10-425-115-91623 (1-985)
QY 5 ProSerHisAProProAlaGluAspArgGluGluAlaGlySerProThrLeuProGlnGly 24
DB 864 CCCCCCACCACCCCCCCCCCCCCCCCCC-----TCCCCCCCCCCCCCCCCCCC 817
QY 25 ProProValProGlyAspProTrpProGlyAlaProProLeuPheGluAspProProPro 44
DB 816 CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCTTCCCAACCCCAACCCCAACCCCAACCC 757
QY 45 ThrArgProSerArgProTrpArgAspLeuProGluThrGlyAlaTrpProProGluPro 64
DB 756 CCCCCCCCCCCCCCCCC-----CCCCCCCCCCCCCCCCCCCCCCCCCCCC 709
QY 65 ProArg-----ThrAspProProGlnProProArgProAspAspProTrpProAlaGly 82
DB 708 CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCAACCAACCCCAACCC 649
QY 83 ProGlnProProGluAsnProTrpProProAlaProGluValAspAsnArgProGlnGlu 102
DB 648 CCCCCCCCCCCCCCCCCCCCCCAACCCCAACCCCAACCCCAACCCCAACCCCAACCC 589
QY 103 GluProAspLeuAspProPro 109
DB 588 CCCCCCCCCCAACCCCTCC 568

RESULT 14
US-09-864-761-20699/c
; Sequence 20699, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wenhseng
; TITLE OF INVENTION: HUMAN GENOME- DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aecmca-X-1
; CURRENT APPLICATION NUMBER: US/09/864, 761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180, 312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207, 456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632, 366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236, 359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234, 687
; PRIOR APPLICATION NUMBER: US 60/234, 687

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/ PRIOR FILING DATE: 2000-09-21
/ PRIOR APPLICATION NUMBER: US 09/608,408
/ PRIOR FILING DATE: 2000-06-30
/ PRIOR APPLICATION NUMBER: US 09/774,203
/ PRIOR FILING DATE: 2001-01-29
/ NUMBER OF SEQ ID NOS: 49117
/ SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
/ SEQ ID NO 20699
/ LENGTH: 446
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ OTHER INFORMATION: MAP TO AC007249.2
/ OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 10
/ OTHER INFORMATION: EXPRESSED IN PETAL LIVER, SIGNAL = 14
/ OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 13
/ OTHER INFORMATION: EXPRESSED IN HEL100, SIGNAL = 12
/ OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 13
/ OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 13
/ OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 12
/ OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 13
/ OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 12
/ OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 9.7
/ OTHER INFORMATION: NT HIT: AL161539.2, EVALUATE 3.70e+00
/ US-09-864-761-20699
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Alignment Scores:
Pred. No.: 2.7e-07 Length: 446
Score: 190.50 Matches: 43
Percent Similarity: 40.00% Conservative: 1
Best Local Similarity: 39.09% Mismatches: 57
Query Match: 27.53% Indels: 9
DB: Gaps: 2
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US-09-994-365-3 (1-114) x US-09-864-761-20699 (1-446)

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QY 5 ProSerHisProProAlaGluAspArgGluGluAlaGlySerProThrLeuProGlnGly 24
Db 403 CCACACACACACACACATCATCCACACACACACACATCATCCACACACACATCA 344
QY 25 ProProValProGlyAspProTTPProGlyAlaProProLeuPheGluAspProPro 44
Db 343 CCACACACACACACATCATCCACACACACACACATCATCCACACACACATCA 284
QY 45 ThrArgProSerArgProTTPArgAspLeuProGluThrGlyValTTPProGluPro 64
Db 283 CCACACACATCATCCACACATCATCATCATCATCA-----CCACACACATCA 236
QY 65 ProArgThrAspProProGlnProProArgProAspAspProTTPProAlaGlyProGln 84
Db 235 CCACATCATCATCCACACACATCATCATCATCATCATCATCATCATCATCA 176
QY 85 ProProGluAsnProTTPPro-----ProAlaProGluValAspAsnArg 99
Db 175 CCACACACACACACATCATCATCATCATCATCATCATCATCATCATCATCATCA 116
QY 100 ProGlnGluGluProAspLeuAspProPro 109
Db 115 CCGCGCGCACACACCGCATCTGCAACCGCA 86
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RESULT 15

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US-10-021-323-5998/c
/ Sequence 5998, Application US/10021323
/ Publication No. US20040123340A1
/ GENERAL INFORMATION:
/ APPLICANT: Delkman, Jill
/ APPLICANT: Feng, Paul C.C.
/ APPLICANT: Fincher, Karen L.
/ APPLICANT: Ziegler, Todd E.
/ TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
/ FILE REFERENCE: 38-21(52274)B
/ CURRENT APPLICATION NUMBER: US/10/021,323
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/ CURRENT FILING DATE: 2001-12-12
/ PRIOR APPLICATION NUMBER: US 60/255, 619
/ PRIOR FILING DATE: 2000-12-14
/ NUMBER OF SEQ ID NOS: 17880
/ SEQ ID NO 5998
/ LENGTH: 420
/ TYPE: DNA
/ ORGANISM: Gossypium hirsutum
/ FEATURE:
/ OTHER INFORMATION: Clone ID: LIB3828-011-Q1-N6-H6
/ US-10-021-323-5998
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Alignment Scores:
Pred. No.: 2.83e-07 Length: 420
Score: 190.00 Matches: 44
Percent Similarity: 39.83% Conservative: 3
Best Local Similarity: 37.29% Mismatches: 57
Query Match: 27.46% Indels: 14
DB: Gaps: 2
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US-09-994-365-3 (1-114) x US-10-021-323-5998 (1-420)

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QY 5 ProSerHisProProAlaGluAspArgGluGluAlaGlySerProThrLeuProGlnGly 24
Db 361 CCCCCGCCCCCCCCGCCCCCCCCGCCCCCCCCCCCCCCCCCCCCCCCCCGAAGC 302
QY 25 ProProValProGlyAspProTTP---ProGlyAlaProProLeuPheGluAspPro--- 42
Db 301 AGCCCCCCCCGCCCCCCCCGCCCCCCCCGCCCCCCCCCCCCCCCCCCCCCCCCC 242
QY 43 -----ProProThrArgProSerArgPro 50
Db 241 CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCGGCC 182
QY 51 ThrArgAspLeuProGluThrGlyValTTPProGluProProArgThrAspProPro 70
Db 181 CCCCCGAGCGCCAGCGCCCAATGCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC 122
QY 71 GlnProProArgProAspAspProTTPProAlaGlyProGlnProProGluAsnProTTP 90
Db 121 CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCGGCC 62
QY 91 ProProAlaProGluValAspAsnArgProGlnGluGluProAspLeuAspPro 108
Db 61 CCCCCCCCCCGGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCCAAGTCCCCCT 8
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Search completed: January 12, 2005, 20:00:09
Job time : 1469 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: January 11, 2005, 11:40:34 ; Search time 2364.82 Seconds
(without alignments)
1756.640 Million cell updates/sec

Title: US-09-994-365-3
Perfect score: 692
Sequence: 1 SEGHPSPHPADREAREASPT.....EVDNRPOEPDLPDPREYR 114

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 32822875 segs, 18219865908 residues
Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODE=frame+g2n.model -DEV=xlh
-Q=cgnt_1/USPTO.epool.h/US0994365/runat_10012005_172232.6834/app.query.fasta_1.590
-DB=EST -QPM=faetap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blomum62 -TRANS=human40.cdi -LIST=45
-DOCLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=prt -NOR=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US0994365 @CGN 1.1.4385 @runat_10012005_172232.6834 -NCPU=6 -ICPU=3
-NO_MAP -LARGEOBURY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -MAIN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6
-Fgapext=7 -YGAPOP=10 -YGAPEXT=0.5 -DELop=6 -DELext=7

Database : EST: *
1: gb_est1: *
2: gb_est2: *
3: gb_hlc: *
4: gb_est3: *
5: gb_est4: *
6: gb_est5: *
7: gb_est6: *
8: gb_gest1: *
9: gb_gest2: *
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	559	80.8	634	7	CF764947 CES003088
2	551	79.6	593	7	CF765720 CES001471
3	541	78.2	383	2	AM315342 12593 MAR
4	507	73.3	416	9	CG481452 OST13885
5	506	73.1	422	1	AT596929 vj46e11.y
6	506	73.1	451	9	CG484009 OST17807
7	506	73.1	669	9	CG484609 OST18617
8	501	72.4	442	9	CG487403 OST22893
9	498	72.0	562	1	AA530301 vj46e11.x

10	471.5	68.1	475	9	CG473878	CG473878 OST1668 M
11	460	66.5	322	9	CG474695	CG474695 OST2738 M
12	446.5	64.5	332	1	AA763309	AA763309 vj98h03.x
13	441	63.7	366	9	CG474680	CG474680 OST2720 M
14	425	61.4	451	1	AA798896	AA798896 vj94e08.x
15	375	54.2	395	9	CG528207	CG528207 OST107284
16	363	52.5	283	9	CG474588	CG474588 OST2599 M
17	345	49.9	243	8	AQ357151	AQ357151 CITRBI-E1-
18	298	43.1	204	1	AA733661	AA733661 vj44f01.x
19	283	40.9	379	1	AA791103	AA791103 vj91a02.x
20	233	33.7	489	8	BH098389	BH098389 RPCT-24-3
21	209	30.2	984	4	BG441224	BG441224 GA_Ea001
22	209	30.2	1380	9	CL058490	CL058490 CH261-82A
23	206	29.8	361	1	AA168568	AA168568 m31c08.x
24	205.5	29.7	812	1	AG133085	AG133085 Pan trogl
25	205	29.6	1272	9	AG356574	AG356574 Mus muscu
26	205	29.6	1283	9	AG435406	AG435406 Mus muscu
27	204.5	29.6	1585	8	CC294035	CC294035 CH261-82A
28	203.5	29.4	977	9	CL488066	CL488066 SATL_503
29	203	29.3	848	9	CNS02YYE	AL220271 Tetradon
30	202.5	29.3	1218	9	AG435362	AG435362 Mus muscu
31	202	29.2	1142	9	CL501710	CL501710 SATL_702
32	201.5	29.1	837	4	BG530104	BG530104 602558771
33	201	29.0	1051	9	CL119109	CL119109 ISB1-75M6
34	201	29.0	2131	8	CC296269	CC296269 CH261-104
35	200.5	29.0	1094	9	CC908599	CC908599 C043p13ba
36	200.5	29.0	1446	9	CL082756	CL082756 CL216-170
37	200	28.9	1648	9	AG390465	AG390465 Mus muscu
38	200	28.9	1691	9	AG341104	AG341104 Mus muscu
39	199.5	28.8	527	9	BX200083	BX200083 BY19125
40	199.5	28.8	609	6	BY719125	BY719125 Pan trogl
41	199.5	28.8	663	9	AG132227	AG132227 Pan trogl
42	199.5	28.8	1331	9	CL490238	CL490238 SATL_534
43	199	28.8	664	9	BX247035	BX247035 Danilo rer
44	199	28.8	964	4	BH416247	BH416247 OP21335 M
45	199	28.8	1038	9	CL478560	CL478560 SATL_292_

ALIGNMENTS

RESULT 1
CF764947
LOCUS
DEFINITION CES003088 Bos taurus skin cDNA library Bos taurus cDNA clone
ACCESSION CF764947 634 bp mRNA linear EST 17-OCT-2003
VERSION CF764947.1 GI:37714166
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus

REFERENCE
AUTHORS Wang, Y.H., McWilliam, S. and Lehnert, S.
TITLE Transcription profiling of cattle skin
JOURNAL Unpublished (2003)
COMMENT Contact: Dr Yonghong Wang
Functional Genomics Lab
CSIRO Livestock Industries
Level 5, Queensland Biosciences Precinct, University of Queensland,
306 Carmody Road St. Lucia QLD Australia
Tel: 07 3214 2445
Fax: 07 3214 2685
Email: Yonghong.Wang@csiro.au
Plate: 40 row: G column: 07.
Location/Qualifiers

FEATURES
source
1..634
/organism="Bos taurus"
/mol_type="mRNA"
/strain="Hereford Shorthorn"
/db_xref="taxon:9913"
/clone="CCL003088"

/sex="female"
/tissue_type="pooled"
/dev_stage="Adult"
/lab_host="XLI-BlueMRF_strain"
/clone_lib="Bos taurus skin cDNA library"
/note="Organ: skin; Vector: Uni-ZAPXR; Site 1: EcoRI;
Site 2: Xho I; Library made from pooled skin of adult
female Hereford-Shorthorn."

ORIGIN

Alignment Scores:

Pred. No.: 7.76e-25 Length: 634
Score: 559.00 Matches: 92
Percent Similarity: 85.09% Conservative: 5
Best Local Similarity: 80.70% Mismatches: 17
Query Match: 80.78% Indels: 0
DB: 7 Gaps: 0

US-09-994-365-3 (1-114) x CF764947 (1-634)

Qy 1 SerGluGlyHisProSerHisProProAlaGluAspArgGluGluAlaGlySerProThr 20

Db 76 AGTGAGAGACCGCTTCCCTCATCCAGAGAGATCTCAGAGAGAGGGCCCTCCACCA 135

Qy 21 LeuProGluGlyProProValProGlyAspProTrpProGlyAlaProProLeuPheGlu 40

Db 136 TTGCTCAGGGCCCCCAATCCCTGGTGACCCCTGGCAGGGGCACCCCGCTTTGAG 195

Qy 41 AspProProProTrpArgProSerArgProTrpArgAspLeuProGluThrGlyValTrp 60

Db 196 GATCTCTCACTCCAGGCCCCCAATCGCTCCGAGAGAGCCTGCTTGTGAGTCTGG 255

Qy 61 ProProGluProProArgTrpAspProGluProGluProProArgProAspAspProTrp 80

Db 256 CCTCTGACCCCTGAGACTGATCCCTCACTCTGCTGCTGCTGCTGCTGCTGCTG 315

Qy 81 AlaGlyProGluProProGluAsnProTrpProProAlaProGluValAspAsnArgPro 100

Db 316 GCAAGACCCCGACCTCCGAGAAACCCCTGGCACCCTGCTGCTGCTGCTGCTGCTG 375

Qy 101 GlnGluGluProAspLeuAspProProArgGluGluTrpArg 114

Db 376 CACGAGAGCCAGACCTTGACCCACGAGGAGAGTACAGA 417

RESULT 2 593 bp mRNA linear EST 17-OCT-2003

LOCUS CF765720 Bos taurus skin cDNA library Bos taurus cDNA clone

ACCESSION CCL001471 5', mRNA sequence.

VERSION CF765720 GI:37714939

KEYWORDS EST.

SOURCE Bos taurus (cow)

ORGANISM Bos taurus

REFERENCE Wang, Y.H., McWilliam, S. and Lehnert, S.

AUTHORS Transcription profiling of cattle skin

JOURNAL Unpublished (2003)

COMMENT Contact: Dr Yonghong Wang

Functional Genomics Lab

CSIRO Livestock Industries

Level 5, Queensland Biosciences Precinct, University of Queensland,

306 Carmody Road St. Lucia QLD Australia

Tel: 07 3214 2445

Fax: 07 3214 2685

Email: Yonghong.Wang@csiro.au

Plate: 25 row: B column: 04.

Location/Qualifiers

1. .593

/organism="Bos taurus"

/mol_type="mRNA"
/strain="Hereford Shorthorn"
/db_xref="taxon:9913"
/clone="CCL001471"
/sex="female"
/tissue_type="pooled"
/dev_stage="Adult"
/lab_host="XLI-BlueMRF_strain"
/clone_lib="Bos taurus skin cDNA library"
/note="Organ: skin; Vector: Uni-ZAPXR; Site 1: EcoRI;
Site 2: Xho I; Library made from pooled skin of adult
female Hereford-Shorthorn."

ORIGIN

Alignment Scores:

Pred. No.: 2.21e-24 Length: 593
Score: 551.00 Matches: 90
Percent Similarity: 86.36% Conservative: 5
Best Local Similarity: 81.82% Mismatches: 15
Query Match: 79.62% Indels: 0
DB: 7 Gaps: 0

US-09-994-365-3 (1-114) x CF765720 (1-593)

Qy 5 ProSerHisProProAlaGluAspArgGluGluAlaGlySerProThrLeuProGluGly 24

Db 88 CTTTCCCTCCATCCAGAGAGATCTCAGAGAGAGGGCCCTCCACCATGGCTCAGGGC 147

Qy 25 ProProValProGlyAspProTrpProGlyAlaProProLeuPheGluAspProProPro 44

Db 148 CCCCACATCCCTGTACCCCTGCGAGGGGCACCCCGCTCTTGTAGAGATCTCCACCT 207

Qy 45 ThrArgProSerArgProTrpArgAspLeuProGluThrGlyValTrpProProGluPro 64

Db 208 CCAAGCCCCATGCTCCGAGAGACTGCTGATTTGAGACTGCTGCTGCTGCTGCTG 267

Qy 65 ProArgThrAspProProGluProProArgProAspAspProTrpProAlaGlyProGlu 84

Db 268 CTTAGAACTGATCCCTCACTCTGCGCTGAGAGAGAGAGAGAGAGAGAGAGAGAG 327

Qy 85 ProProGluAsnProTrpProProAlaProGluValAspAsnArgProGluGluPro 104

Db 328 CTTCCAGAAACCCCTGCGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 387

Qy 105 AspLeuAspProProArgGluGluTrpArg 114

Db 388 GACCTTGACCCACCCAGAGAGAGTACAGA 417

RESULT 3 383 bp mRNA linear EST 09-JUL-2000

LOCUS AM315342 Sus scrofa cDNA 5', mRNA sequence.

ACCESSION AM315342

VERSION AM315342.1 GI:6744598

KEYWORDS EST.

SOURCE Sus scrofa (pig)

ORGANISM Sus scrofa

REFERENCE Wang, Y.H., McWilliam, S. and Lehnert, S.

AUTHORS Transcription profiling of cattle skin

JOURNAL Unpublished (2003)

COMMENT Contact: Dr Yonghong Wang

Functional Genomics Lab

CSIRO Livestock Industries

Level 5, Queensland Biosciences Precinct, University of Queensland,

306 Carmody Road St. Lucia QLD Australia

Tel: 07 3214 2445

Fax: 07 3214 2685

Email: Yonghong.Wang@csiro.au

Plate: 25 row: B column: 04.

Location/Qualifiers

1. .593

/organism="Bos taurus"

Email: smtch@mail.marc.usda.gov
Single pass sequencing. Bases called and trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 20
and -mismatch 12 options.

PCR Primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCCTCAGTCAGCAG
Plate: 8 row: A column: 14
Seq primer: ATTAGGTGACCTATAG.

FEATURES
Source Location/Qualifiers
1..383

/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/tissue_type="pooled"
/lab_host="DH10B"
/clone_id="MARC 2PTG"
/note="Vector: pCMV SPORT6; site_1: NotI; site_2: SalI;
library made from pooled tissue from testis, ovary,
endometrium, hypothalamus, pituitary, and placenta."

ORIGIN

Alignment Scores:
Pred. No.: 5,72e-24 Length: 383
Score: 541.00 Matches: 87
Percent Similarity: 86.24% Conservative: 7
Best Local Similarity: 79.82% Mismatches: 15
Query Match: 78.18% Indels: 0
DB: 2 Gaps: 0

US-09-994-365-3 (1-114) x AW315342 (1-383)

Qy 1 SerGluGlyHisProSerHisProProAlaGluAspArgGluGluAlaGlySerProThr 20
Db 57 AGCGAAGACCAACCATCTCCCAATCCACGAGGCTTCAGAGGAGGCTCCCAACA 116
Qy 21 LeuProGlnGlyProProValProGlyAspProTyrProGlyAlaProProLeuPheGlu 40
Db 117 TTGGCTGGGGCCCCCAATCCCGGTGACCTTGCGCAGGGGTACTCTCATTTTGAG 176
Qy 41 AspProProThrArgProSerArgProTyrArgAspLeuProGluThrGlyValTyr 60
Db 177 GACCTCTCAGCTCCAGGCCCCAATCTGCTCCGAGAGACCTGCTGATCTGAGTCTGG 236
Qy 61 ProProGluProProAlaGlyThrAspProProGlnProProArgProAspAspProTyr 80
Db 237 CCTCTTAACCCCTAGTACTGATCCCTCTCACTCCCGCTGACGACCTCTGACCA 296
Qy 81 AlaGlyProGlnProProGluAsnProTyrProProAlaProGluValAspAsnArgPro 100
Db 297 GCAGGACCCCAAGCTCCAGAAACCTCTGCGCACCTGCTGAGTGTGACCAAGATCC 356
Qy 101 GlnGluGluProAspLeuAspProPro 109
Db 357 CGAGAGAGCCAGACCTTGACCCACC 383

RESULT 4
LOCUS CG481452 416 bp DNA linear GSS 01-OCT-2003
DEFINITION OST13885 Mus musculus 129Sv/Ev Mus musculus genomic clone, OST13885,
genomic survey sequence.
ACCESSION CG481452
VERSION CG481452.1 GI:37233834
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 416)
Zambrowicz, B.P., Abuin, A., Ramirez-Solis, R., Richter, L.J.,
Figueroa, J., Beltrami, R., Buxton, E.C., Edwards, J., Finch, R.A.,
Fridde, C.J., Gupta, A., Hansen, G., Hu, Y., Huang, W., Jaling, C.,
Key, B.W., Jr., Kipp, P., Kohlhauff, B., Ma, Z.-Q., Markesich, D.,

TITLE Payne, R., Potter, D.G., Qian, N., Shaw, J., Schrick, J., Shi, Z.-Z.,
Sparke, M.J., Van Sligtenhorst, I., Vogel, P., Walke, W., Xu, N.,
Zhu, O., Person, C. and Sands, A.T.
JOURNAL Wnt1 kinase deficiency lowers blood pressure in mice: a gene-trap
screen to identify potential targets for therapeutic intervention
COMMENT Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
Contact: Zambrowicz BP
OmniBank

Lexicon Genetics Incorporated
4000 Research Forest Drive, The Woodlands, TX 77381, USA
Email: materials@lexgen.com
Gene trap sequence tag generated by 3' RACE from mouse ES cells as
described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
Class: Gene Trap.

FEATURES

Source Location/Qualifiers
1..416
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="129Sv/Ev"
/db_xref="taxon:10090"
/clone="OST13885"
/cell_type="embryonic stem cell"
/clone_id="Mus musculus 129Sv/Ev"

ORIGIN

Alignment Scores:
Pred. No.: 7.16e-22 Length: 416
Score: 507.00 Matches: 80
Percent Similarity: 82.14% Conservative: 12
Best Local Similarity: 71.43% Mismatches: 20
Query Match: 73.27% Indels: 0
DB: 9 Gaps: 0

US-09-994-365-3 (1-114) x CG481452 (1-416)

Qy 3 GlyHisProSerHisProProAlaGluAspArgGluGluAlaGlySerProThrLeuPro 22
Db 14 GCGACCTCTTCCCGGATCTACAGACACCGAAGAGAGACTCCCAACATTCCT 73
Qy 23 GlnGlyProProValProGlyAspProTyrProGlyAlaProProLeuPheGluAspPro 42
Db 74 CTGGAGACCCCAATCCCTGTGTATCCCTGGCTGGGGCGCTCTTGTGTGATGAACCT 133
Qy 43 ProProThrArgProSerArgProTyrArgAspLeuProGluThrGlyValTyrProPro 62
Db 134 CCGCTCTCAAGCTTCAACCGTCTCTGAGAGATCTTCTGACATGTGCTGCCCCCA 193
Qy 63 GluProProArgThrAspProProGlnProProArgProAspAspProTyrProAlaGly 82
Db 194 AAGCCCCCAAGCACTGATCCCTGAACCTCTGTGCTATGACCTGCGCAGAGGA 253
Qy 83 ProGlnProProGluAsnProTyrProProAlaProGluValAspAsnArgProGlnGlu 102
Db 254 ACCCAGCCCCCAGAAACCTCTGCGCTCTGCGCTCTGAGATGAGCATTGATCTCAGAG 313
Qy 103 GluProAspLeuAspProProArgGluGluTyrArg 114
Db 314 GAGCCAGACCTTGACCCACCCAGAAAGATATAGA 349

RESULT 5
LOCUS A1596929 422 bp mRNA linear EST 21-APR-1999
DEFINITION v146e11.y1 Stragene mouse skin (#937313) Mus musculus cDNA clone
IMAGE:932108 5', mRNA sequence.
ACCESSION A1596929
VERSION A1596929.1 GI:4605977
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 422)
Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T.,

Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritters, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
The WashU-NCI Mouse EST Project 1999
Unpublished (1999)
Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.edu
This clone is available royalty-free through LML; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
MG1:537028

FEATURES
SOURCE
This read is a RESSEQUENCE of a previously sequenced mouse clone
correct orientation
Seq primer: -40RP from Glibco
High quality sequence stop: 396.
Location/Qualifiers
1..422
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:932108"
/sex="females"
/tissue_type="whole skin"
/dev_stage="11 weeks old"
/lab_host="SOLR (kanamycin resistant)"
/clone_id="Stratagene mouse skin (#93713)"
/note="Organ: skin; Vector: pBluescript SK-; Site: 1:
EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer:
Oligo dT. Whole skin from 11 week old C57BL/6 female mice.
Average insert size: 1.0 kb; Uni-ZAP XR Vector: -5'
adaptor sequence: 5' GAATTCGACGAG 3' -3' adaptor
sequence: 5' CTCGAGTTTCTTTTCTTTT 3'."

ORIGIN

Alignment Scores:
Pred. No.: 8,35e-22 Length: 422
Score: 506.00 Matches: 80
Percent Similarity: 82.14% Conservat: 12
Best Local Similarity: 71.43% Mismatches: 20
Query Match: 73.12% Indels: 0
DB: 1 Gaps: 0
US-09-994-365-3 (1-114) x AT596929 (1-422)

QY 3 G1YHISPROSErHISProProAlaGluAspArgGluGluAlaGlySerProThrIeuPro 22
Db 41 GGGGACCTTCTCCCGATCTACAGACACCCAGAAAGAGAGACTCCCACTTGCCT 100
QY 23 G1NGLYProProValProGlyAspProTTPProGlyAlaProIeuPheGluAspPro 42
Db 101 CTGGGACCCCAATCCCTGGTGAATCCCTGGGCTGGGCGGCTCTTGTGTGAATGAACCT 160
QY 43 ProProThrArgProSerArgProTTPArgAspIeuProGluThrGlyValTTPProPro 62
Db 161 CCGGCTTCAGAGCTCCACCGTCCCTGGAGAGATCTTCTTCAAGTGTGCTGCTGCCCA 220
QY 63 GluProProArgThrAspProProGlnProProArgProAspAspProTTPProAlaGly 82
Db 221 AAGCCCCCAAGCACTATCTCCCTTAACCTCTCTGCTGATGACCCCTGCGAGAGCA 280
QY 83 ProGlnProProGluAsnProTTPProProAlaProGlyValAspAsnArgProGlnGlu 102
Db 281 ACCGACGCCCCAGAAACCCCTGGCTCTGCGCCCTGAGATGAGACATGATCTCAGAG 340
QY 103 GluProAspIeuAspProProAlaArgGluGluTyrArg 114
Db 341 GAGCCAGACCTTACCCACCCAGAGAGAGATATAGA 376

RESULT 6
CG484009
LOCUS
DEFINITION
CG484009 451 bp DNA linear GSS 01-OCT-2003
OST17807 Mus musculus 129Sv/Ev Mus musculus genomic clone OST17807,
genomic survey sequence.
ACCESSION
CG484009
VERSION
CG484009.1 GI:37239343
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)

REFERENCE
AUTHORS
Zambrowicz, B.P., Abuin, A., Ramirez-Solis, R., Richter, L.J.,
Piggott, J., Beltrande-Rio, H., Buxton, E.C., Edwards, J., Finch, R.A.,
Fridde, C.J., Gupta, A., Hansen, G., Hu, Y., Huang, W., Jating, C.,
Key, B.W., Jr., Kipp, P., Kohlhauf, B., Ma, Z.-Q., Markesich, D.,
Payne, R., Potter, D.G., Qian, N., Shaw, J., Schlick, J., Shi, Z.-Z.,
Sparks, M.J., Van Slighemhorst, I., Vogel, P., Walke, W., Xu, N.,
Zhu, Q., Person, C. and Sands, A.T.
Mkn1 kinase deficiency lowers blood pressure in mice: a gene-trap
screen to identify potential targets for therapeutic intervention
Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
Contact: Zambrowicz BP
Omnibank

FEATURES
SOURCE
Lexicon Genetics Incorporated
4000 Research Forest Drive, The Woodlands, TX 77381, USA
Email: materials@lexgen.com
Gene trap sequence tag generated by 3' RACE from mouse ES cells as
described in Zambrowicz et al (Nature, 1998 Apr 9;392(6676):608-11)
Class: Gene Trap.
Location/Qualifiers
1..451
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="129Sv/Ev"
/db_xref="taxon:10090"
/clone="OST17807"
/cell_type="embryonic stem cell"
/clone_id="Mus musculus 129Sv/Ev"

ORIGIN

Alignment Scores:
Pred. No.: 8,94e-22 Length: 451
Score: 506.00 Matches: 80
Percent Similarity: 82.14% Conservat: 12
Best Local Similarity: 71.43% Mismatches: 20
Query Match: 73.12% Indels: 0
DB: 9 Gaps: 0
US-09-994-365-3 (1-114) x CG484009 (1-451)

QY 3 G1YHISPROSErHISProProAlaGluAspArgGluGluAlaGlySerProThrIeuPro 22
Db 15 GGGGACCTTCTCCCGATCTACAGACACCCAGAAAGAGAGACTCCCACTTGCCT 74
QY 23 G1NGLYProProValProGlyAspProTTPProGlyAlaProIeuPheGluAspPro 42
Db 75 CTGGGACCCCAATCCCTGGTGAATCCCTGGGCTGGGCGGCTCTTGTGTGAATGAACCT 134
QY 43 ProProThrArgProSerArgProTTPArgAspIeuProGluThrGlyValTTPProPro 62
Db 135 CCGGCTTCAGAGCTCCACCGTCCCTGGAGAGATCTTCTGACAGTGTGCTGCGCCCA 194
QY 63 GluProProArgThrAspProProGlnProProArgProAspAspProTTPProAlaGly 82
Db 195 AAGCCCCCAAGCACTATCTCCCTTAACCTCTCTGCTGATGAGACCCCTGCGAGAGCA 254
QY 83 ProGlnProProGluAsnProTTPProProAlaProGlyValAspAsnArgProGlnGlu 102
Db 255 ACCGACGCCCCAGAAACCCCTGGCTCTGCGCCCTGAGATGAGACATGATCTCAGAG 314

0Y 103 G|U|P|r|o|a|b|l|e|a|s|p|r|o|f|r|o|a|g|l|u|g|l|u|T|y|r|a|g 114
 Db 315 G|A|G|C|C|A|G|A|C|T|T|G|A|C|C|C|C|G|A|G|A|G|A|T|A|G|A 350

RESULT 7
 CG484609 669 bp DNA linear GSS 01-OCT-2003
 LOCUS CG484609
 DEFINITION OST118617 Mus musculus 129Sv/Ev Mus musculus genomic clone OST18617,
 genomic survey sequence.
 ACCESSION CG484609
 VERSION CG484609.1 GI:37240590
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 669)
 REFERENCE Zambrowicz, B. P., Abuhin, A., Ramirez-Solis, R., Richter, L. J.,
 Piagotti, J., Beltrandello, H., Buxton, E. C., Edwards, J., Finch, R. A.,
 Fridele, C. U., Gupta, A., Hansen, G., Hu, Y., Huang, W., Jaing, C.,
 Key, B. W., Jr., Kipp, P., Kohlhaufl, B., Ma, Z.-Q., Markesich, D.,
 Payne, R., Potter, D. G., Qian, N., Shaw, J., Schrick, J., Shi, Z.-Z.,
 Sparks, M. J., Van Sligtenhorst, I., Vogel, P., Walke, W., Xu, N.,
 Zhu, Q., Pearson, C. and Sande, A. T.
 Wnt1 kinase deficiency lowers blood pressure in mice: a gene-trap
 screen to identify potential targets for therapeutic intervention
 Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
 COMMENT Contact: Zambrowicz BP
 OmniBank

TITLE
 JOURNAL
 CONTACT: Zambrowicz BP

FEATURES
 source
 location/Qualifiers
 1..669
 /organism="Mus musculus"
 /mol_type="Genomic DNA"
 /strain="129Sv/Ev"
 /db_xref="taxon:10090"
 /clone="OST18617"
 /cell_type="embryonic stem cell"
 /clone_lib="Mus musculus 129Sv/Ev"

ORIGIN
 Alignment Scores:
 Pred. No.: 1,34e-21 Length: 669
 Score: 506.00 Matches: 80
 Percent Similarity: 82.14% Conservative: 12
 Best Local Similarity: 71.43% Mismatch: 20
 Query Match: 73.12% Indels: 0
 Db: 9 Gaps: 0

US-09-994-365-3 (1-114) x CG484609 (1-669)
 0Y 3 G|Y|H|I|S|P|r|o|S|e|r|H|A|S|P|r|o|P|r|o|A|G|U|A|S|H|A|S|P|r|g|l|u|a|g|l|u|a|g|l|u|S|e|r|P|r|o|T|H|r|e|u|P|r|o 22
 Db 8 G|G|C|G|A|C|C|T|T|C|C|G|G|A|T|C|A|C|A|G|A|C|C|C|A|G|A|G|A|G|A|G|A|G|A|T|G|C|C|G|C|C|A|C|A|T|T|G|C|T 67
 0Y 23 G|I|N|G|I|Y|P|r|o|P|r|o|v|a|l|P|r|o|G|I|Y|A|S|P|P|r|o|T|P|r|o|G|I|Y|A|A|P|r|o|F|r|o|e|u|P|h|e|u|S|p|r|o 42
 Db 68 C|T|G|G|A|C|C|C|C|A|A|T|C|C|T|G|G|A|T|C|C|T|G|G|C|C|T|G|G|G|G|G|G|C|C|T|C|T|T|G|T|T|G|A|T|G|A|A|C|T 127
 0Y 43 P|r|o|P|r|o|T|H|r|A|S|P|r|o|S|e|r|A|S|P|r|o|T|P|r|o|T|P|r|A|S|H|A|S|P|r|o|G|I|U|T|H|G|I|V|A|T|P|r|o|P|r|o 62
 Db 128 C|G|G|C|T|C|A|G|G|T|C|C|A|C|C|G|T|C|C|T|G|G|A|G|A|T|C|T|C|T|G|A|C|A|G|T|G|C|C|T|G|G|C|C|C|C|C|C|A 187
 0Y 63 G|U|P|r|o|P|r|o|A|g|T|H|A|S|P|r|o|P|r|o|G|I|U|I|N|P|r|o|P|r|o|A|T|P|r|o|A|S|H|A|S|P|r|o|T|P|r|o|A|a|g|l|y 82
 Db 188 A|A|G|C|C|C|C|A|G|A|G|A|C|G|A|T|C|C|C|C|T|A|A|C|T|C|T|G|C|C|T|G|A|T|G|A|C|C|C|T|G|G|C|C|A|G|A|G|A 247
 0Y 83 P|r|o|G|I|U|I|N|P|r|o|G|I|U|A|S|H|A|S|P|r|o|T|P|r|o|P|r|o|A|A|P|r|o|G|I|U|A|A|S|H|A|S|P|r|o|G|I|U|I 102

Db	248	ACCCAGCCCCCAGAAACCCTTGGCTTCCTGCTCCCTTGATGACGACATGATCTCAGAG	307
Oy	103	GluProApeLueAppProProArgGluGluYrArg	114
Db	308	GAGCCAGACTTGACCCCAAGAGATATAGA	343
RESULT 8			
CG487403			
DEFINITION	CG487403 Mus musculus 129Sv/Ev Mus musculus genomic clone OST2893.	442 bp DNA linear GSS 01-OCT-2003	
ACCESSION	OST2893		
VERSION	CG487403		
KEYWORDS	CG487403.1 GI:37246315		
SOURCE	GSS.		
ORGANISM	Mus musculus (house mouse)		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Scurionathi; Muridae; Murinae; Mus.		
AUTHORS	1 (bases 1 to 442) Zambrowicz,B.P., Abidin,A., Ramirez-Solis,R., Richter,L.J., Pigott,J., BeltrandeRio,H., Buxton,E.C., Edwards,J., Finch,R.A., Fridde,C.J., Gupta,A., Hansen,G., Hu,Y., Huang,W., Jaing,C., Key,B.W., Jr., Kipp,P., Kohlhauff,B., Ma,Z.-Q., Markesich,D., Payne,R., Potter,D.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.-Z., Spake,M.J., Van Sligtenhorst,I., Vogel,P., Walke,W., Xu,N., Zhu,Q., Person,C. and Sands,A.T. Mml kinase deficiency lowers blood pressure in mice: a gene-trap screen to identify potential targets for therapeutic intervention Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003) Contact: Zambrowicz BP		
TITLE	OmitBank		
JOURNAL	Lexicon Genetics Incorporated 4000 Research Forest Drive, The Woodlands, TX 77381, USA Email: materials@lexgen.com		
COMMENT	Gene trap sequence tag generated by 3' RACE from mouse ES cells as described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):600-11) Class: Gene Trap. Location/Qualifiers		
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	/organism="Mus musculus"		
	/mol_type="Genomic DNA"		
	/strain="129Sv/Ev"		
	/db_xref="taxon:10090"		
	/clone="OST2893"		
	/cell_type="embryonic stem cell"		
	/clone_lib="Mus musculus 129Sv/Ev"		
ORIGIN			
Alignment Scores:			
Pred. No.:	1.76e-21	Length:	442
Score:	501.00	Matches:	79
Percent Similarity:	82.73%	Conservative:	12
Best Local Similarity:	71.82%	Mismatches:	19
Query Match:	72.40%	Indels:	0
DB:	9	Gaps:	0
US-994-365-3 (1-114) x CG487403 (1-442)			
Oy	5	ProSeRHiSPProPfoAlaGluaSPArGiLuGluAlaGlySerProThLeuProGlnGly	24
Db	4	CCTCTCCCGGATCTACAGACACCACAGAAAGAGAGACTCCACCATTTGCCTGTGGGA	63
Oy	25	ProProValAProGlyAAPProTriProGlyValAProProLeuAPheGluAAPProProPro	44
Db	64	CCCCCAATCCCTGTGATCCTTGCGCTGGGGCGCTCTCTTTTGTGATGAACCTCGGCT	123
Oy	45	ThrArgProSeRaArgProTriPaArgASpieuBroGluThrGlyValITProProGluPro	64
Db	124	CCAGGCTCAACCGTCCCTGAGAGATCTTCTGACAAGTGTGCTGCGCCCAAGGCC	183
Oy	65	ProAtgHTrAPPProProGlnInProProArgProAspAspProTTPProAlaGlyProGln	84

Db	184	CCAAACACTGATCCCCCTTAAACCTCCTCTGCTGTATGACCCCTGGCAGACGAAACCCAG	243
Qy	85	ProProgluAspProTyrProProba1aProgluVlaAspAsnArgProGlnIngluPro	104
Db	244	CCCCGAGAAACCCCTGGCTCTCTGCTGCTGTAGATGACCATGAATCTCAGAGAGACCA	303
Qy	105	AspLeuAspProProArgIngluTyrArg	114
Db	304	GACCTTGACCCACCCGAGAGATATAGA	333
RESULT 9			
AA530301			
LOCUS			
DEFINITION	AA530301	562 bp mRNA	linear EST 22-JUL-1997
ACCESSION	AA530301	IMAGE:332108 5', mRNA sequence.	Mus musculus cDNA clone
VERSION	AA530301.1		
KEYWORDS	EST.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
REFERENCE	EuKaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 562)		
AUTHORS	Marra,M., Hillier,L., Allen,M., Bowles,M., Dierich,N., Dubouque,T., Geisler,S., Kucaba,T., Lacy,M., Le,M., Martin,U., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theisinger,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.		
TITLE	The WashU-HHMI Mouse EST Project		
JOURNAL	Unpublished (1996)		
COMMENT	Contact: Marra M/Mouse EST Project WashU-HHMI Mouse EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: mouseest@watson.wustl.edu This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MG1:537028 Seq primer: -28m13 rev1 ET from Amersham High quality sequence stop: 221. Location/Qualifiers		
FEATURES			
source	1..562		
	/organism="Mus musculus"		
	/mol_type="mRNA"		
	/strain="C57BL/6"		
	/db_xref="taxon:10090"		
	/clone="IMAGE:932108"		
	/sex="females"		
	/tissue_type="whole skin"		
	/dev_stage="11 weeks old"		
	/lab_host="SOLR (Ranamyxin resistant)"		
	/clone_11b="Stratagene mouse skin (#937313)"		
	/note="Organ: skin; Vector: pBluescript SK-; Site 1: EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer: Oligo dt. Whole skin from 11 week old C57BL/6 female mice Average insert size: 1.0 kb; Uni-ZAP XR Vector; ~5' adaptor sequence: 5' GAATTCGCGACGAG 3'-3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'."		
ORIGIN			
Alignment Scores:			
Pred. NO.:	3,42e-21	Length:	562
Score:	498.00	Matches:	79
Percent Similarity:	81.25%	Conservative:	12
Best Local Similarity:	70.54%	Mismatches:	21
Query Match:	71.97%	Indels:	0
DB:	1	Gaps:	0
US-09-994-365-3 (1-114) x AA530301 (1-562)			
Yy	3	GlyHisProSerHisProProAlaGluAspArgGluGluAlaGlySerProThrLeuPro	22

Db 40 GGGCAACCTTCTCCGGATCTACACACCCACGAAGGAGAGACTCCCCACCATTTGCT 99
QY 23 GlnGlyProProValProGlyAspProTrpProGlyAlaProProLeuPheGluAspPro 42
Db 100 CTGGACCCCCCAATCTCCGTGATCCCTGGCTGGGGGGCCCTCTTTGTTATCAACT 159
QY 43 ProProThrArgProSerArgProTrpArgAspLeuProGluValThrGlyValTrpProPro 62
Db 150 CCGCTCCAGGCTCCACCGTCGCTCGAGAGATCTTCTGACAGTGGTCTGGGCCCA 219
QY 63 GluProArgGlnAspProProGlnInProProArgProAspAspProTrpProAlaGly 82
Db 220 AAGCCCCAAGACTGATCCCCCTAACTCCTGCTGATGACCCCTGGCCAGAGGA 279
QY 83 ProGlnProProGluAsnProTrpProProAlaProGluValAspAsnArgProGlnGlu 102
Db 280 ACCCAGCCCCAGAAACCCCTGGCTCTGCCCCGTGAGATGACCATGAATCTCAGAG 339
QY 103 GluProAspLeuAspProProArgGluGlnTrpArg 114
Db 340 GAGCCAGACTTGAACCAACCAAGAAAGTGTAA 375

RESULT	10
LOCUS	CG473878
DEFINITION	CG473878 Mus musculus 129Sv/Ev Mus musculus genomic clone OST1668,
ACCESSION	OST1668 Mus musculus 129Sv/Ev Mus musculus genomic survey sequence.
VERSION	CG473878
KEYWORDS	CG473878.1 GI:37224767
SOURCE	GSS.
ORGANISM	Mus musculus (house mouse)
REFERENCE	Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciuromorphi; Muridae; Murinae; Mus. 1 (bases 1 to 475) Zambrowicz, B.P., Abuhin, A., Ramirez-Solis, R., Richner, L.J., Piggott, J., BeltrandelRio, H., Buxton, E.C., Edwards, J., Finch, R.A., Fridde, C.J., Gupta, A., Hansen, G., Hu, Y., Huang, W., Jaijg, C., Key, B.W., Jr., Klipp, P., Konhauf, B., Ma, Z.-Q., Markesich, D., Payne, R.J., Potter, D.G., Qian, N., Shaw, J., Schrick, J., Shi, Z.-Z., Sparks, M.J., Van Sligtenhorst, I., Vogel, P., Walke, W., Xu, N., Zhu, Q., Person, C. and Sands, A.T. Wnt1 kinase deficiency lowers blood pressure in mice: a gene-trap screen to identify potential targets for therapeutic intervention Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003) Contact: Zambrowicz BP
JOURNAL	OmiBank
COMMENT	Lexicon Genetics Incorporated 4000 Research Forest Drive, The Woodlands, TX 77381, USA Email: materials@lexgen.com Gene trap sequence tag generated by 3' RACE from mouse ES cells as described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11). Class: Gene Trap.
FEATURES	Location/Qualifiers
source	1..475 /organism="Mus musculus" /mol_type="genomic DNA" /strain="129Sv/Ev" /db_xref="taxon:10090" /clone="OST1668" /cell_type="embryonic stem cell" /clone_lib="Mus musculus 129Sv/Ev"
ORIGIN	
Alignment Scores:	
Pred. No.:	1.16e-19 Length: 475
Score:	471.50 Matches: 74
Percent Similarity:	80.37% Conservative: 12
Best Local Similarity:	69.16% Mismatches: 16
Query Match:	68.14% Indels: 5
DB:	Gaps: 1

US-09-994-365-3 (1-114) x CG473878 (1-475)

Qy 7 HisProProAlaGluAspArgGluGluAlaGlySerProThrLeuProGlnGlyProPro 26
 Db 40 CACCCA-----CGAAGAGAGATCCCAACCATTCCTCTGGAGACCCCA 84
 Qy 27 ValProGlyAspProTyrProGlyValAlaProPheLeuPheGluAspProProProthra 46
 Db 85 ATCCCTGGATGATCCCTGGCTGGGGCGGCTCTTGTGTGTGTGATGAACCTTCGGCTCAAGC 144
 Qy 47 ProSerArgProTyrArgAspLeuProGluThrGlyValTyrProProGluProProArg 66
 Db 145 TCACAACGCTCCCTGGAGAGATCTTCTGACAGTGTGCTGGCCCCCAAGCCCCCAAGC 204
 Qy 67 ThrAspProProGlnProProArgProAspAspProTyrProAlaGlyProGlnProPro 86
 Db 205 ACTGATCCCTCTAAACCTCTCTGCTGATGACCCCTGGCAGCAGAACCAACGACCCCA 264
 Qy 87 GluAsnProTyrProProAlaAlaProGluValAlaAspAsnArgProGlnGluGluProAspLeu 106
 Db 265 NAAACACCCCTGGCTCTGCTGGAGAAATGACCATGATCTCAGAGAGAGCANAACTT 324
 Qy 107 AspProProArgGluGluTyr 113
 Db 325 GACCCACCCCAAGAAANTAT 345

RESULT 11
 CG474695 322 bp DNA linear GSS 01-OCT-2003
 LOCUS OSR2738 Mus musculus 1295v/Ev Mus musculus genomic clone OSR2738,
 DEFINITION genomic survey sequence.
 ACCESSION CG474695
 VERSION CG474695.1 GI:37225584
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 322)
 Zambrowicz,B.P., Abuin,A., Ramirez-Solis,R., Richter,L.J.,
 Piegott,J., BeltrandelRio,H., Buxton,E.C., Edwards,J., Finch,R.A.,
 Fritdile,C.J., Gupta,A., Hansen,G., Hu,Y., Huang,W., Jaing,C.,
 Key,B.W., Kipp,P., Kohhauff,B., Ma,Z.-Q., Matkeich,D.,
 Payne,R., Potter,D.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.-Z.,
 Sparks,M.J., Van Slightenhorst,I., Vogel,P., Walke,W., Xu,N.,
 Zhu,Q., Person,C. and Sande,A.T.
 Wnt1 kinase deficiency lowers blood pressure in mice: a gene-trap
 screen to identify potential targets for therapeutic intervention
 Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
 CONTACT: Zambrowicz BP
 OMNIBANK

JOURNAL
 COMMENT
 Lexicon Genetics Incorporated
 4000 Research Forest Drive, The Woodlands, TX 77381, USA
 Email: materials@lexgen.com
 Gene trap sequence tag generated by 3' RACE from mouse B5 cells as
 described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
 Class: Gene Trap.
 Location/Qualifiers
 1..322
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="129Sv/Ev"
 /db_xref="taxon:10090"
 /clone="OSR2738"
 /cell_type="embryonic stem cell"
 /clone_11b="Mus musculus 129Sv/Ev"

ORIGIN
 Alignment Scores:
 Pred. No.: 3,89e-19 Length: 322
 Score: 460.00 Matches: 74
 Percent Similarity: 82.35% Conservative: 10
 Best Local Similarity: 72.55% Mismatch: 17

Query Match:	66.47%	Indels:	1
DB:	9	Gaps:	0

US-09-994-365-3 (1-114) x CG474695 (1-322)
 QY 14 GUGUUAAGIAGSERTPOTHLNPPROGLNGLYPROBVOALPROGlyASPProTTPPro 33
 ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
 Db 6 AAAGAAGAGACCTCCCAACATTGCCCTGTGGAGACCCCAATCCTGGTGATCCCTGGCGCT 65
 QY 34 GLyAaProPLeuPheGLuaSPPrOPrOThraArProSerArPTOTPyASp 53
 ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
 Db 66 GGGCGCGCTCTTTGTTGAATGAACCTCCGCTCCAGACTCAACCTGCCTCGAGAGAT 125
 QY 54 LeuPProGLunHrGLyValTTPPrOPrOGLuPPrOBraKgrHrrAPPrOPrOGlnPrOPro 73
 ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
 Db 126 CTTCTTAGACMTGTGTGCTGGCCCCCAAGCCCCCAAGACTGATCCCCTAAACCTCT 185
 QY 74 ArProASPaAPPPrOTTPPrOAAGLyProGLInPrOPrOGLuaSPnPTTPPrOProAla 93
 ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
 Db 186 CTGCTGATGACCCTTGCCAGACGAGAACCCAGCCCCCANAAAAACCTGCTTCGCC 245
 QY 94 ProGLuVALaPaPaMaArGTPrOGInGLuGLuProASpleuASpPro-BroArGTGLuJutY 113
 ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
 Db 246 CCTGAGATGAGCCNTGANTCTCAGAGAGAGCCANAACCTTGAACCAACCCAGGAGAAAGTA 305
 QY 113 TAQT 114
 |||
 Db 306 TAGA 309

RESULT 12
 AA763309 332 bp mRNA linear EST 27-JAN-1998
 LOCUS vW99h03.r1 StrataGene mouse skin (#937313) Mus musculus cDNA clone
 DEFINITION IMAGE:1229621 5', mRNA sequence.
 AA763309
 ACCESSION AA763309.1 GI:2813056
 VERSION
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 332)
 AUTHORS Matra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
 Geisel,S., Kucada,T., Lacy,M., Le,M., Martin,J., Morris,M.,
 Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
 Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
 Waterston,R.
 TITLE The WashU-HMI Mouse EST Project
 JOURNAL Unpublished (1996)
 COMMENT Contact: Marra M/Mouse EST Project
 WashU-HMI Mouse EST Project
 Washington University School of Medicine
 444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@watsn.wustl.edu
 This clone is available royalty-free through LIND / contact the
 IMAGE Consortium (info@image.lind.gov) for further information.
 MGI:655213
 Seq primer: -28ml3 rev1 ET from Amershams
 High quality sequence stop: 329.
 Location/Qualifiers
 1..332
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6"
 /db_xref="taxon:10090"
 /clone="IMAGE:1229621"
 /sex="females"
 /tissue type="whole skin"
 /dev_stage="11 weeks old"
 /lab_host="SOLR (kanamycin resistant)"
 /clone_id="Stratagene mouse skin (#937313)"

ORIGIN

/note="Organ: skin; Vector: pBluescript SK-; Site 1: EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer: Oligo dT. Whole skin from 11 week old C57BL/6 female mice. Average insert size: 1.0 kb; Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATTCGACGAG 3' -3' adaptor sequence: 5' CTCGAGTTTCTTTTCTTTT 3'."

Alignment Scores:

Score:	2.64e-18	Length:	332
Percent Similarity:	44.50	Matches:	77
Best Local Similarity:	81.48%	Conservative:	11
Query Match:	71.30%	Mismatches:	15
	64.52%	Indels:	7
		Gaps:	1

US-09-994-365-3 (1-114) x AA763309 (1-332)

QY 7 HisProProAlaGluAspArgGluGluAlaGlySerProThrLeuProGlnGlyProPro 26
 Db 3 CACCCA-----CGAAGAGAGAGACTCCACCATTTGCTCGGAGACCCCA 47
 QY 27 ValProGlyAspProTTPProGlyAlaProProLeuPheGluAspProProProThrArg 46
 Db 48 ATCCCTGATGATCCCTGCGGCGGGG--CTTCCTTTGTTGATGAACCTCCGCTCC--AGG 105
 QY 47 ProSerArgProTTPArgAspLeuProGluThrGlyValTTPProProGluProProArg 66
 Db 106 TCCAACGCTCCCTGAGAGATCTTCGACAGTGTGCTGCGGCCCCCAAGCCCCCAAGC 165
 QY 67 ThrAspProProGlnProProArgProAspAspProTTPProAlaGlyProGlnProPro 86
 Db 166 ACTGATCCCTTAACCTCCTGCTGATGATGACCTCGGCGAGAGAACCCCAACCCCA 225
 QY 87 GluAsnProTTPProProAlaProGluValAspAsnArgProGlnGluGluProAspLeu 106
 Db 226 GAAACCCCTGCGCTCTGCGCCCTGAGATGACCATGATCTCAGAGAGGCCGACCTT 285
 QY 107 AspProProArgGluGluTyrArg 114
 Db 286 GACCAACCCCAAGAGATATAGA 309

RESULT 13
 LOCUS CG474680 386 bp DNA linear GSS 01-OCT-2003
 DEFINITION OSM2720 Mus musculus 129sv/Er Mus musculus genomic clone OSM2720,
 genomic survey sequence.
 ACCESSION CG474680
 VERSION CG474680.1 GI:37225569
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 386)
 Zambrowicz,B.P., Abuin,A., Ramirez-Solis,R., Richter,L.J.,
 Piggott,D., BeltrandeRio,H., Buxton,B.C., Edwards,J., Finch,R.A.,
 Fiddle,C.J., Gupta,A., Hansen,G., Hu,Y., Huang,W., Jaling,C.,
 Key,B.W., Jr., Kipp,P., Kohlhauff,B., Ma,Z.-Q., Markesich,D.,
 Payne,R., Potter,D.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.-Z.,
 Sparks,M.J., Van Sligtenhorst,L., Vogel,P., Walke,W., Xu,N.,
 Zhu,Q., Person,C. and Sands,A.T.
 Wku kinase deficiency lowers blood pressure in mice: a gene-trap
 screen to identify potential targets for therapeutic intervention

TITLE Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
 JOURNAL CONTACT: Zambrowicz BP
 COMMENT OmniBank

Lexicon Genetics Incorporated
 4000 Research Forest Drive, The Woodlands, TX 77381, USA
 Email: materials@lexgen.com
 Gene trap sequence tag generated by 3' RACE from mouse ES cells as
 described in Zambrowicz et al (Nature. 1998 Apr 9;352(6676):608-11)
 Class: Gene trap.

FEATURES
 source

Location/Qualifiers
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 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="129sv/Er"
 /db_xref="taxon:10090"
 /clone="OST2720"
 /cell_type="embryonic stem cell"
 /clone_1lb="Mus musculus 129sv/Er"

ORIGIN

Alignment Scores:
 Pred. No.: 6.64e-18 Length: 386
 Score: 441.00 Matches: 68
 Percent Similarity: 75.45% Conservative: 15
 Best Local Similarity: 61.82% Mismatches: 27
 Query Match: 63.73% Indels: 0
 DB: Gaps: 0

US-09-994-365-3 (1-114) x CG474680 (1-386)

QY 5 ProSerHisProProAlaGluAspArgGluGluAlaGlySerProThrLeuProGlnGly 24
 Db 7 CCTTCTCCGATCTACAGACACCACAAAAGAGAGACTCCACCATTTGCTCGGGA 66
 QY 25 ProProValProGlyAspProTTPProGlyAlaProProLeuPheGluAspProProPro 44
 Db 67 CCCCAATCCCTGATCCCTGCGGCGGCTCTTTGTTGATNAACCTCGGCT 126
 QY 45 ThrArgProSerArgProTTPArgAspLeuProGluThrGlyValTTPProProGluPro 64
 Db 127 CAGAGCTCCACCGCTCCTGAGANAGATCTTCGACANTGTGCTCGGCCCCCAAGCCC 186
 QY 65 ProArgThrAspProProGlnProProArgProAspAspProTTPProAlaGlyProGln 84
 Db 187 CNAAGCTGATCCCTTAACCTCCTGCTGCTNATNACCCTGCGCAGAGAGACCAN 246
 QY 85 ProProGluAsnProTTPProProAlaProGluValAspAsnArgProGlnGluGluPro 104
 Db 247 CCCCAGAAAAACCCCTGCGCTCTGCGCCCTGAATGATGACCATGATCTCAGAGAGGCCA 306
 QY 105 AspLeuAspProProArgGluTyrArg 114
 Db 307 AACCTTGACCCNCCCAAGAAATATATAA 336

RESULT 14
 LOCUS AA798896 451 bp mRNA linear EST 10-FEB-1998
 DEFINITION vv94e08.r1 StrataGene mouse skin (#937313) Mus musculus cDNA clone
 IMAGE:1230086 5', mRNA sequence.
 ACCESSION AA798896
 VERSION AA798896.1 GI:2861851
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 451)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

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 Scheinberg,K., Stepien,M., Tan,F., Underwood,K., Moore,B.,
 Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
 Waterston,R.

TITLE The WashU-HMI Mouse EST Project
 JOURNAL Unpublished (1996)
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